

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) Publication number: **0 667 393 A2**

(12)

EUROPEAN PATENT APPLICATION

(21) Application number: 95100438.1

(51) Int. Cl.⁶: C12N 15/10, C12Q 1/68

(22) Date of filing: 13.01.95

(30) Priority: 13.01.94 US 182621

(43) Date of publication of application:
16.08.95 Bulletin 95/33

(94) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IE IT LI LU MC
NL PT SE

(71) Applicant: ENZO DIAGNOSTICS, INC.
60 Executive Boulevard
Farmingdale,
New York 11735-4716 (US)

(72) Inventor: Engelhardt, Dean L
173 Riverside Drive (No. 19A)
New York,
New York 10025 (US)

Inventor: Stavrianopoulos, Jannis G.
99 South Clinton (No.11D)
Bay Shore,
New York 11706 (US)

Inventor: Rabbani, Elazar
69 Fifth Avenue (No. 19A)
New York,
New York 10003 (US)

Inventor: Donegan, James J.
210 East Broadway (No. 3G)
Long Beach,
New York 11561 (US)

(74) Representative: VOSSIUS & PARTNER
Siebertstrasse 4
D-81675 München (DE)

(54) Novel process, construct and conjugate for producing multiple nucleic acid copies.

(57) This invention provides *inter alia* an *in vitro* process for producing multiple specific nucleic acid copies in which the copies are produced under isostatic conditions, e.g., temperature, buffer and ionic strength, and independently of any requirement for introducing an intermediate structure for producing the copies. In other aspects, the invention provides *in vitro* processes for producing multiple specific nucleic acid copies in which the products are substantially free of any primer-coded sequences, such sequences having been substantially or all removed from the product to regenerate a primer binding site, thereby allowing new priming events to occur and multiple nucleic acid copies to be produced. This invention further provides a promoter-independent non-naturally occurring nucleic acid construct that produces a nucleic acid copy or copies without using or relying on any gene product that may be coded by the nucleic acid construct. Another aspect of this invention concerns a protein-nucleic acid construct in the form of a conjugate linked variously, e.g., covalent linkage, complementary nucleic acid base-pairing, nucleic acid binding proteins, or ligand receptor binding. Further disclosed in this invention is an *in vivo* process for producing a specific nucleic acid in which such a protein-nucleic acid construct conjugate is introduced into a cell. A still further aspect of the invention relates to a construct comprising a host promoter, second promoter and DNA sequence uniquely located on the construct. The host transcribes a sequence in the construct coding for a different RNA polymerase which after translation is capable of recognizing its cognate promoter and transcribing from a DNA sequence of interest in the construct with the cognate promoter oriented such that it does not promote transcription from the construct of the different RNA polymerase.

EP 0 667 393 A2

This invention relates to the field of *in vitro* and *in vivo* production of nucleic acid production and to nucleic constructs and protein-nucleic acid conjugates for use in such production.

All patents, patent publications, scientific articles, and videocassettes cited or identified in this application are hereby incorporated by reference in their entirety in order to describe more fully the state of the art to which the present invention pertains.

Current methodology cited heretofore in the literature relating to amplification of a specific target nucleic acid sequence *in vitro* essentially involve 2 distinct elements:

1. repeated strand separation or displacement or a specific "intermediate" structure such as a promoter sequence linked to the primer or introduction an assymetric restriction site not originally present in the nucleic acid target; followed by
2. production of nucleic acid on the separated strand or from an "intermediate" structure.

Separation can be accomplished thermally or by enzymatic means. Following this separation, production is accomplished enzymatically using the separated strands as templates.

Of the established amplification procedures, Polymerase Chain Reaction (PCR) is the most widely used. This procedure relies on thermal strand separation, or reverse transcription of RNA strands followed by thermal dissociation. At least one primer per strand is used and in each cycle only one copy per separated strand is produced. This procedure is complicated by the requirement for cycling equipment, high reaction temperatures and specific thermostable enzymes. (Saiki, et al., Science 230:1350-1354 (1985); Mullis and Faloona, Methods in Enzymology 155: 335-351 (1987); U.S. Patent Nos. 4,683,195 and 4,883,202).

Other processes, such as the Ligase Chain Reaction (LCR) (Backman, K., European Patent Application Publication No. 0 320 308; Landegren, U., et al. Science 241 1077 (1988); Wu, D. and Wallace, R.B. Genomics 4 560 (1989); Barany, F. Proc. Nat. Acad. Sci USA 88:189 (1991)), and Repair Chain Ligase Reaction (RLCR) or Gap Ligase Chain Reaction (GLCR) (Backman, K. et al. (1991) European Patent Application Publication No. 0 439 182 A; Segev, D. (1991) European Patent Application Publication No. 0 450 594) also use repeated thermal separation of the strands and each cycle produces only one ligated product. These procedures are more complicated than PCR because they require the use of an additional thermostable enzyme such as a ligase.

More complicated procedures are the Nucleic Acid Sequence Based Amplification (NASBA) and Self Sustained Sequence Reaction (3SR) amplification procedures. (Kwoh, D.Y. et al., Proc Nat Acad Sci., USA., 86:1173-1177 (1989); Guatelli, J.C. et al., 1990 Proc Nat Acad Sci., USA 87:1874-1878 (1990) and the Nucleic Acids Sequence Based Amplification (NASBA) (Kievits, T., et al J. Virol. Methods 35:273-286 (1991); and Malek, L.T., U.S. Patent No. 5,130,238). These procedures rely on the formation of a new "intermediate" structure and an array of different enzymes, such as reverse transcriptase, ribonuclease H, T7 RNA polymerase or other promotor dependant RNA polymerases and they are further disadvantaged by the simultaneous presence of ribo- and deoxyribonucleotide triphosphates precursors.

For the intermediate construct formation, the primer must contain the promotor for the DNA dependent RNA polymerase. The process is further complicated because the primer is, by itself, a template for the RNA polymerase, due to its single-stranded nature.

The last of the major amplification procedures is Strand Displacement Amplification (SDA) (Walker, G.T. and Schram, J.L., European Patent Application Publication No. 0 500 224 A2; Walker, G.T. et al. European Patent Application No. 0 543 612 A2; Walker, G.T., European Patent Application Publication No. 0 497 272 A1; Walker, G.T. et al., Proc Natl Acad Sci USA 89:392-396 (1992); and Walker, G.T. et al., Nuc Acids Res. 20:1691-1696 (1992)). The intermediate structure of this procedure is formed by the introduction of an artificial sequence not present in the specific target nucleic acid and which is required for the assymetric recognition site of the restriction enzyme. Again this procedure involves more than one enzyme and the use of thio nucleotide triphosphate precursors in order to produce this assymetric site necessary for the production step of this amplification scheme.

The random priming amplification procedure (Hartley, J.L., U.S. Patent No. 5,043,272) does not relate to specific target nucleic acid amplification.

Probe amplification systems have been disclosed which rely on either the amplification of the probe nucleic acid or the probe signal following hybridization between probe and target. As an example of probe amplification is the Q-Beta Replicase System (Q β) developed by Lizardi and Kramer and their colleagues. Q β amplification is based upon the RNA-dependent RNA polymerase derived from the bacteriophage Q β . This enzyme can synthesize large quantities of product strand from a small amount of template strand, roughly on the order of 10⁶ to 10⁹ (million to billion) increases. The Q β replicase system and its replicatable RNA probes are described by Lizardi et al., "Exponential amplification of recombinant RNA hybridization probes," Biotechnology 6:1197-1202 (1988); Chu et al., U.S. Patent No. 4,957,858; and well as by Keller and Manak (DNA Probes, MacMillan Publishers Ltd, Great Britain, and Stockton Press (U.S. and Canada,

1989, pages 225-228). As discussed in the latter, the Q β replicase system is disadvantaged by non-specific amplification, that is, the amplification of non-hybridized probe material, which contributes to high backgrounds and low signal-to-noise ratios. Such attendant background significantly reduces probe amplification from its potential of a billion-fold amplification to something on the order of 10⁴ (10,000 fold). In addition, the Q beta amplification procedure is a signal amplification - and not a target amplification.

In vivo

Literature covering the introduction of genes or antisense nucleic acids into a cell or organism is very extensive (Larrick, J.W. and Burck, K. Gene Therapy Elsevier Science Publishing Co., Inc, New York (1991); Murray, J.A.H. ed Antisense RNA and DNA, Wiley-Liss, Inc., New York (1992)). The biological function of these vectors generally requires inclusion of at least one host polymerase promoter.

The present invention as it relates to *in vitro* and *in vivo* production of nucleic acids is based on novel processes, constructs and conjugates which overcome the complexity and limitations of the above-mentioned documents.

The present invention provides an *in vitro* process for producing more than one copy of a specific nucleic acid in which the process is independent of any requirement for the introduction of an intermediate structure for the production of the specific nucleic acid. The process comprises three steps, including (a) providing a nucleic acid sample containing or suspected of containing the sequence of the specific nucleic acid; (b) contacting the sample with a three component reaction mixture; and (c) allowing the mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing more than one copy of the specific nucleic acid. The reaction mixture comprises: (i) nucleic acid precursors, (ii) one or more specific nucleic acid primers each of which is complementary to a distinct sequence of the specific nucleic acid, and (iii) an effective amount of a nucleic acid producing catalyst.

In another aspect, the present invention provides an *in vitro* process for producing more than one copy of a specific nucleic acid in which the products are substantially free of any primer-coded sequences. Such a process comprises the following steps, including (a) providing a nucleic acid sample containing or suspected of containing the sequence of the specific nucleic acid; (b) contacting the sample with a three component mixture (the mixture comprising (i) nucleic acid precursors, (ii) one or more specific polynucleotide primers comprising at least one ribonucleic acid segment each of which primer is substantially complementary to a distinct sequence of the specific nucleic acid, and (iii) an effective amount of a nucleic acid producing catalyst); and (c) allowing the mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of the specific nucleic acid; and (d) removing substantially or all primer-coded sequences from the product produced in step (c). By removing such sequences, a primer binding site is regenerated, thereby allowing a new priming event to occur and producing more than one copy of the specific nucleic acid.

The present invention also provides an *in vitro* process for producing more than one copy of a specific nucleic acid in which the products are substantially free of any primer-coded sequences. In the steps of this process, said process comprising a nucleic acid sample containing or suspected of containing the sequence of the specific nucleic acid is provided, and contacted with a reaction mixture. The mixture comprises (i) unmodified nucleic acid precursors, (ii) one or more specific chemically-modified primers each of which primer is substantially complementary to a distinct sequence of said specific nucleic acid, and (iii) an effective amount of a nucleic acid producing catalyst. The mixture thus contacted is allowed to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of the specific nucleic acid. In a further step, substantially or all primer-coded sequences from the product produced in the reacting step is removed to regenerate a primer binding site. The regeneration of a primer binding site thereby allows a new priming event to occur and the production of more than one copy of said specific nucleic acid.

An additional provision of the present invention is an *in vitro* process for producing more than one copy of a specific nucleic acid in which the products are substantially free of any primer-coded sequences. In this instance, the process comprises the steps of: (a) providing a nucleic acid sample containing or suspected of containing the sequence of the specific nucleic acid; and (b) contacting the sample with a reaction mixture (the mixture comprising (i) unmodified nucleic acid precursors, (ii) one or more specific unmodified primers comprising at least segment each of which primer comprises at least one non-complementary sequence to a distinct sequence of the specific nucleic acid, such that upon hybridization to the specific nucleic acid, at least one loop structure is formed, and (iii) an effective amount of a nucleic acid producing catalyst). The mixture so formed is allowed to react in step (c) under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of the specific nucleic acid;

which step is followed by (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site. The regeneration of a primer binding site thereby allows a new priming event to occur and the production of more than one copy of said specific nucleic acid.

Another embodiment of the present invention concerns a promoter-independent non-naturally occurring nucleic acid construct which when present in a cell produces a nucleic acid without the use of any gene product coded by the construct.

In yet another embodiment, the present invention provides a conjugate comprising a protein-nucleic acid construct in which the nucleic acid construct does not code for said protein, and which conjugate produces a nucleic acid when present in a cell.

The present invention also has significant *in vivo* applications. In one such application, an *in vivo* process is provided for producing a specific nucleic acid. The *in vivo* process comprises the steps of (a) providing a conjugate comprising a protein-nucleic acid construct, the conjugate being capable of producing a nucleic acid when present in a cell; and (b) introducing such a conjugate into a cell, thereby producing the specific nucleic acid.

Another significant aspect of the present invention relates to a construct comprising a host promoter located on the construct such that the host transcribes a sequence in the construct coding for a different RNA polymerase, which after translation is capable of recognizing its cognate promoter and transcribing from a DNA sequence of interest from the construct with the cognate promoter oriented such that it does not promote transcription from the construct of the different RNA polymerase.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 (A-F) depicts various nucleic acid construct forms contemplated by the invention in which at least one single-stranded region are located therein.

Figure 2 (A-F) depicts the functional forms of the nucleic acid constructs illustrated in Figure 1 (A-F).

Figure 3 (A-C) is an illustration of three nucleic acid constructs with an RNA polymerase covalently attached to a transcribing cassette.

Figure 4 (A-C) illustrates three nucleic acid constructs with promoters for endogenous RNA polymerase.

Figure 5 is a nucleic acid sequence for M13mp18.

Figure 6 shows the sequence and the positions of the primers derived from M13mp18 which were employed in the present invention for nucleic acid production.

Figure 7 illustrates appropriate restriction sites in M13mp18.

Figure 8 is an agarose gel with a lane legend illustrating the experimental results in Example 5 in which amplification of the M13 fragment was carried out in the presence of a large excess (1500 fold) of irrelevant DNA.

Figure 9 is an agarose gel with a lane legend illustrating the results in Example 8 in which the effect of variations of reaction conditions on the product obtained in Example 3 was investigated.

Figure 10 is an agarose gel with a lane legend that illustrates the results of a qualitative analysis of the effects observed in Example 9 of various buffers on the amplification reaction in accordance with the present invention.

Figure 11 is a southern blot (with lane legend) obtained from Example 10 in which two buffers, DMAB and DMG, were separately employed in nucleic acid production.

Figure 12 is an agarose gel and lane legend obtained in Example 11 in which the nature of the ends of amplified product was investigated.

Figure 13 is an agarose gel obtained in Example 12 in which amplification from non-denatured template was examined.

Figure 14 is an agarose gel obtained in Example 13 in which amplification from an RNA template was examined.

Figure 15 is a southern blot of the gel obtained in Figure 14.

Figure 16 is a fluorescence spectrum illustrating the results obtained in Example 14 in which the phenomenon of "strand displacement" using ethidium-labeled oligonucleotides in accordance with the present invention was investigated.

Figure 17 is a fluorescence spectrum illustrating the results obtained in Example 15 in which a T7 promoter oligonucleotide 50 mer labeled with ethidium was employed to study its effects on *in vitro* transcription by T7 and T3 polymerases from an IBI 31 plasmid (pIBI 31-BH5-2) and from a BlueScript II plasmid construct (pBSII/HCV).

Figure 18 depicts the polylinker sequences of the IBI 31 plasmid (pIBI 31-BH5-2) and the BlueScript II plasmid construct (pBSII/HCV).

The present invention describes novel methods and constructs for production of multiple copies of specific nucleic acid sequences *in vitro* and *in vivo*

One aspect of this invention represents an *in vitro* process for the production of more than one copy of nucleic acid from specific target nucleic acid (either DNA or RNA) sequences utilizing a biological catalyst, e.g., a DNA polymerase, primer oligonucleotides complementary to sequences (primer sites) in the target nucleic acid. The production process can proceed in the presence of a large excess of other nucleic acids and does not require thermal cycling or the introduction of specific intermediate constructs such as promoters or asymmetric restriction sites, etc.

More particularly, this invention provides an *in vitro* process for producing more than one copy of a specific nucleic acid, the process being independent of a requirement for the introduction of an intermediate structure for the production of any such specific nucleic acid. The *in vitro* production process comprises the steps of: (a) providing a nucleic acid sample containing or suspected of containing the sequence of the specific nucleic acid; (b) contacting the sample with a three component mixture; and (c) allowing the thus-contacted mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing more than one copy of the specific nucleic acid. The three component mixture just alluded will generally comprise (i) nucleic acid precursors, (ii) one or more specific nucleic acid primers each of which is complementary to a distinct sequence of the specific nucleic acid, and (iii) an effective amount of a nucleic acid producing catalyst. In other aspects, the specific nucleic acid may be single-stranded or double-stranded, and may take the form of deoxyribonucleic acid, ribonucleic acid, a DNA:RNA hybrid or a polymer capable of acting as a template for a nucleic acid polymerizing catalyst.

In addition, the specific nucleic acid can be in solution in which case the above-described *in vitro* process may further comprise the step of treating the specific nucleic acid with a blunt-end promoting restriction enzyme. Further, isolation or purification procedures can be employed to enrich the specific nucleic acid. Such procedures are well-known in the art, and may be carried out on the specific nucleic acid prior to the contacting step (b) or the reacting step (c). One means of isolation or purification of a nucleic acid involves its immobilization, for example, by sandwich hybridization (Ranki et al., 1983), or sandwich capture. Particularly significant in the latter methodology is the disclosure of Engelhardt and Rabbani, U.S. Patent Application Serial No. 07/968,706, filed on October 30, 1992, entitled "Capture Sandwich Hybridization Method and Composition," now allowed, that was published as European Patent Application Publication No. 0 159 719 A2 on October 30, 1985. The contents of the foregoing U.S. patent application is incorporated herein by reference.

The target nucleic acid can be present in a variety of sources. For purposes of disease diagnosis these would include blood, pus, feces, urine, sputum, synovial fluid, cerebral spinal fluid, cells, tissues, and other sources. The production process can be performed on target nucleic acid that is present in samples which are free of interfering substances, or the production process can be performed on target nucleic acid separated from the sample. The nucleic acid can be in solution or bound to a solid support. While the replication process can be carried out in the presence of nonrelevant nucleic acids, certain applications may require prior separation of the target sequences. Methods such as sandwich hybridization or sandwich capture referenced above can then be applied to immobilize target sequences. In such instances where sandwich hybridization or sandwich capture is carried out, the above-described *in vitro* process may further comprise the step of releasing the captured nucleic acid, e.g., by means of a restriction enzyme.

As described above, the target sequence need not be limited to a double-stranded DNA molecule. Target molecules could also be single stranded DNA or RNA. For example, replication of a single-stranded target DNA could proceed using primers complementary to both the single-stranded DNA target and to the produced complementary sequence. Following the initial synthesis of the complementary sequence DNA, production from this strand would begin. RNA can serve as the template using a DNA polymerase I, e.g., Klenow, which can reverse transcribe under conditions that have been described (Karkas, J.D. et al., Proc Nat Acad Sci U.S.A. 69:398-402 (1972)).

In case the target nucleic acid is double stranded, a restriction digest or sonication, partial endonuclease treatment or denaturation could be employed for the preparation of the target nucleic acid before the onset of amplification.

An aspect of this invention concerns its use in determining whether a specific target nucleic acid was derived from a living or a deceased organism. To make such a determination, one could in parallel amplify and detect the presence of a specific target DNA or a specific target RNA associated with the genomic makeup of the organism; and thereafter amplify and detect the presence of a specific RNA target associated to the biological function (living function) of the organism which does not survive if the organism is deceased.

The nucleic acid precursors contemplated for use in the present invention are by and large well-known to those skilled in the art. Such precursors may take the form of nucleoside triphosphates and nucleoside triphosphate analogs, or even combinations thereof. More particularly, such nucleoside triphosphates are selected from deoxyadenosine 5'-triphosphate, deoxyguanosine 5'-triphosphate, deoxythymidine 5'-triphosphate, deoxycytidine 5'-triphosphate, adenosine 5'-triphosphate, guanosine 5'-triphosphate, uridine 5'-triphosphate and cytidine 5'-triphosphate, or a combination of any of the foregoing. Such nucleoside triphosphates are widely available commercially, or they may be synthesized by techniques or equipment using commercially available precursors.

In the case where the nucleic acid precursors comprise nucleoside triphosphate analogs, these are also widely available from a number of commercial sources, or they may be manufactured using known techniques. Such nucleoside triphosphate analogs can be in the form of naturally occurring or synthetic analogs, or both.

It should not go unrecognized or even unappreciated that the foregoing nucleoside triphosphate and nucleoside triphosphate analogs can be unmodified or modified, the latter involving modifications to the sugar, phosphate or base moieties. For examples of such modifications, see Ward et al., U.S. Patent No. 4,711,955; Engelhardt et al., U.S. Patent No. 5,241,060; Stavrianopoulos, U.S. Patent No. 4,707,440; and Wetmur, Quartin and Engelhardt, U.S. Patent Application Serial No. 07/499,938, filed on March 26, 1990, the latter having been disclosed in European Patent Application Serial No. 0 450 370 A1, published on October 9, 1991. The contents of the foregoing U.S. patents and patent application are incorporated by their entirety into the present application.

The primers, one or more, described herein bind to specific sequences on the target nucleic acids and initiate the polymerizing reaction. While oligo deoxynucleotide primers may be preferred, polydeoxynucleotide as well as oligo and polyribonucleotide or nucleotide copolymer primers can be used (Kornberg, A. and T. A. Baker, second edition, 1992, W.H. Freeman and Co. New York, Karkas, J.D., PNAS 69:2288-2291 (1972); and Karkas, J.D. et al., Proc. Natl. Acad. Sci. U.S.A. 69:398-402 (1972)). Thus, the specific nucleic acid primers may be selected from deoxyribonucleic acid, ribonucleic acid, a DNA:RNA copolymer, or a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization. Under conditions where the primer is an oligoribonucleotide or copolymer, the primer can be removed from its cognate binding site using specific enzymatic digestion (e.g., RNase H, restriction enzymes and other suitable nucleases) such that another primer can bind and initiate synthesis. This can be used as a system for the multiple initiation of the synthesis of polynucleotide or oligonucleotide product.

Modifications, including chemical modifications, in the composition of the primers would provide for several novel variations of the invention. See, for example, U.S. Patent Nos. 4,711,955; 5,241,060; 4,707,440; and U.S. Patent Application Serial No. 07/499,938, *supra*. For example, substitution of the 3' hydroxyl group of the primer by an isoteric configuration of heteroatoms, e.g., a primary amine or a thiol group, would produce chemically cleavable linkers. In the case of thiol excess of another thiol in the reaction mixture will cleave the phosphorothioate linkers which is formed after the initiation of polymerization, thus allowing the DNA polymerase to reinitiate polymerization with the same primer. Thus, in this variation repeated syntheses can begin from a modified, hybridized primer providing a significant increase in the synthesis of DNA.

In another aspect of the invention, the specific nucleic acid primers are not substantially complementary to one another, having for example, no more than five complementary base-pairs in the sequences therein.

In another variation, the primer could contain some noncomplementary sequences to the target, whereupon hybridization would form at least one loop or bubble which could be used as a substrate for a specific endonuclease such that the primer could be removed from the target by enzymatic digestion thus allowing reinitiation. Furthermore, the primer could contain additional sequences noncomplementary to the target nucleic acid. Thus, the specific nucleic acid primers may comprise at least one non-complementary nucleotide or nucleotide analog base, or at least one sequence thereof. The range of non-complementarity may range in some cases from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs, and in other cases, from about 5 to about 20 nucleotides. Such noncomplementary base sequence or sequences can be linked by other than a phosphodiester bond.

As used herein, the term "nucleic acid producing catalyst" is intended to cover any agent, biological, physical or chemical in nature, that is capable of adding nucleotides (e.g., nucleoside triphosphates, nucleoside triphosphate analogs, etc.) to the hydroxyl group on the terminal end of a specific primer (DNA or RNA) using a pre-existing strand as a template. A number of biological enzymes are known in the art which are useful as polymerizing agents. These include, but are not limited to *E. coli* DNA polymerase I, Klenow polymerase (a large proteolytic fragment of *E. coli* DNA polymerase I), bacteriophage T7 RNA

polymerase, and polymerases derived from thermophilic bacteria, such as Thermus aquaticus. The latter polymerase are known for their high temperature insensitivity, and include, for example, the *Taq* DNA polymerase I. A thermostable *Taq* DNA polymerase is disclosed in Gelfand et al., U.S. Patent No. 4,889,818. Preferred as a polymerizing agent in the present invention is the *Taq* DNA Polymerase I. Many if not all of the foregoing examples of polymerizing agents are available commercially from a number of sources, e.g., Boehringer-Mannheim (Indianapolis, IND). Particularly suitable as nucleic acid producing catalysts are DNA polymerase and reverse transcriptase, or both. As used herein, "the effective amount" of the nucleic acid producing catalyst is an art-recognized term reflecting that amount of the catalyst which will allow for polymerization to occur in accordance with the present invention.

Since the rate and extent of hybridization of the primers is dependent upon the standard conditions of hybridization (Wetmur, J.G. and Davidson, N. J., Mol. Biol. 31:349 (1968)), the concentration and nucleotide sequence complexity of the total primers added to the reaction mixture will directly affect the rate at which they hybridize and accordingly the extent to which they will initiate nucleic acid synthesis. In addition, if the reaction is run under conditions where the guanosine triphosphate is replaced by inosine triphosphate or other modified nucleoside triphosphates such that the presence of this modified nucleotide in the product nucleic acid would lower the melting temperature of the product:template double helix, then at any given temperature of the reaction the extent of breathing of the double helix will be increased and the extent of binding of the primers to the target strand will be enhanced.

Furthermore, primers could displace the strands at the ends of the double stranded target and hybridize with one of the two strands and, this displacement hybridization reaction (or D loop formation reaction) is favored by adding more than one primer molecule. In general, as the total amount of the sequence complexity of the primers complementary to the target nucleic acid is increased a greater nucleic acid production is obtained (see Example 3 below).

Modification of the primers could either increase or decrease the binding of primer to the target at a given pH, temperature and ionic strength, in other words, at isostatic conditions of pH, temperature and ionic strength, e.g., ionic salt. Other primer modifications can be employed which would facilitate polymerization from the primer sites, even when the initiation site is within a double helix. For example, once an oligo primer is introduced into a target double stranded nucleic acid molecule, if such an oligo primer is modified with ethidium or any moiety that increases the melting temperature of the double stranded structure formed by the oligo and a target nucleic acid, it forms a relatively more stable single stranded structure because of the nucleotide modifications. This produces a primer initiation site. In fact, the nucleic acid precursors or the specific primers (or both) can be modified by at least one intercalating agent, such as ethidium, in which case it may be useful to carry out an additional step (d) of detecting any product produced in step (c), as set forth above. In such a step where desirable, detection can be carried out by means of incorporating into the product a labeled primer, a labeled precursor, or a combination thereof.

Another additional aspect of the *in vitro* process, above-described, is the inclusion of a further step of regenerating one or more specific nucleic acid primers, as described elsewhere in this disclosure, including immediately below.

As described in the summary of this invention, an *in vitro* process for multiple nucleic acid production is provided in which the products are substantially free of any primer-coded sequences. In such process, the removing step (d) is carried out by digestion with an enzyme, e.g., ribonuclease H. In one aspect of this invention, the nucleic acid precursors are modified or unmodified in the instance where one or more specific polynucleotide primers are used, the primers comprising at least one ribonucleic acid segment and wherein each primer is substantially complementary to a distinct sequence of the specific nucleic acid. Thus, the specific polynucleotide primers may further comprise deoxyribonucleic acid. In another feature of this particular *in vitro* process, the specific polynucleotide primers contain a 3'-hydroxyl group or an isoteric configuration of heteroatoms, e.g., nitrogen, sulfur, or both. In addition, the polynucleotide primers in this instance may further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.

In yet a further *in vitro* process for producing more than one copy of a specific nucleic acid is provided (as described in the summary), the products being substantially free of any primer-coded sequences. In this instance, unmodified nucleic acid precursors are reacted in a mixture with one or more chemically-modified primers each of which is substantially complementary to a distinct sequence of the specific nucleic acid. An effective amount of a nucleic acid producing catalyst is also provided in the mixture. As in the case of the last-described *in vitro* process, the removing step (d) may be carried out by digestion with an enzyme, e.g., ribonuclease H. The specific chemically modified primers are selected, for example, from ribonucleic acid, deoxyribonucleic acid, a DNA:RNA copolymer, and a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization, or a combination of any of the foregoing.

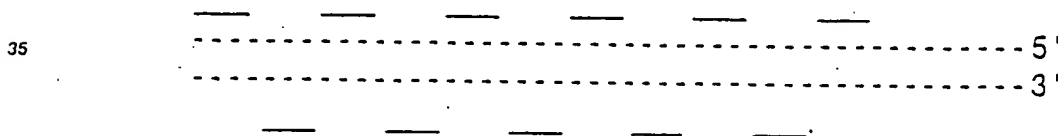
The specific chemically modified primers may contain a 3'-hydroxyl group or an isosteric configuration of heteroatoms, N, S, or both, as described above in other *in vitro* processes. Further, the specific chemically modified primers can be selected from nucleoside triphosphates and nucleoside triphosphate analogs, or a combination thereof, wherein at least one of said nucleoside triphosphates or analogs is modified on the sugar, phosphate or base. Also as in other *in vitro* processes, the specific chemically modified primers may further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.

In still yet another of the *in vitro* processes for multiple nucleic acid production, described previously in the summary of this invention, unmodified nucleic acid precursors are provided in the mixture and reacting step (c), together with one or more specific unmodified primers comprising at least one segment, each of which primer comprises at least one non-complementary sequence to a distinct sequence of the specific nucleic acid, such that upon hybridization to the specific nucleic acid at least one loop structure is formed. As in the other instances, digestion with an enzyme, e.g., ribonuclease H, may be employed in the removing step (d). In one feature of this process, specific unmodified primers are selected from ribonucleic acid, deoxyribonucleic acid, a DNA:RNA copolymer, and a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization, or a combination of any of the foregoing. Further, the specific unmodified primers may further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs, in accordance with the present invention.

The rate of hybridization of the primer to target nucleic acids and, in particular, to target double stranded nucleic acids can be facilitated by binding of the primer with various proteins, e.g., rec A proteins. For example, if the primer is modified with an intercalating agent, e.g., ethidium (or any moiety that increases the melting temperature of the double stranded structure), the addition of this primer to or with a protein such as rec A, either free or bound, would facilitate the introduction of the primer into the double stranded target. (Kornberg and Baker, *supra*, pages 797-800). This could produce a suitable primer initiation site.

The arrangement of primer binding sites on the template nucleic acid can be varied as desired. For example, the distance between successive primer binding sites on one strand can also be varied as desired. Also specific primers can be employed that initiate synthesis upstream of the sequence sought to be copied. Under this scenario, multiple copies of nucleic acid are made without successive denaturation or use of other enzymes or the introduction of intermediate structures for their production.

When primer sites on double stranded DNA are arranged as shown, specific DNA production is increased.



When the target sequences are substantially covered by their complementary primers, a further increase in the production of multiple copies of nucleic acid is favored due to the increase in initiation points and destabilization of the double stranded template molecule.

Finally, if an oligo is modified such that it will form a stable hybrid, even in the presence of the complementary nucleic acid strand, then the modified oligo can act as a 'helper' oligo. 'Helper' oligo in this context is defined as a oligo that does not necessarily act as a primer but will accelerate the binding and priming activity of other oligos in the vicinity to the binding site of the 'helper' oligo. Vicinity is here being defined as the location of a nucleotide sequence or the complementary nucleotide sequence close enough to the binding site of the 'helper' oligo to have the rate or extent of hybridization of the primer affected by the binding of the 'helper' oligo. The 'helper' oligo can be modified such that it does not initiate polymerization as for example through the use of a dideoxy 3' terminal nucleotide or other nucleotide with blocked 3' ends. The 'helper' oligo can also be modified in such a manner that the double helix formed by the 'helper' oligo and the target nucleic acid strand or the 'helper' and the complementary strand to the target strand is more stable or has a higher melting temperature than the equivalent double helix of unmodified 'helper' oligo and the target or the strand complementary to the target strand. Such modifications can include halogenation of certain bases, ethenyl pyrimidines (C:C triple bonds, propyne amine derivatives; the addition of ethidium or other intercalating molecules (see Stavrianopoulos and Rabbani, U.S. Patent Application Serial No. 07/956,566, filed on October 5, 1992, the contents of which are incorporated herein by reference and which were disclosed in European Patent Application Publication No. 0 231 495 A2,

published on August 12, 1987); the supplementation of the oligo with certain proteins that stabilize the double helix and any other treatment or procedure or the addition of any other adduct that serves to stabilize the portion of the double helix with the 'helper' bound or to increase the melting temperature of portion of the double helix with the 'helper' bound.

5

In vivo Synthesis of Nucleic Acid

This invention describes a cassette or nucleic acid construct into which any nucleic acid sequence can be inserted and which can be used as a template for the production of more than one copy of the specific
 10 sequence. This cassette is a nucleic acid construct containing a sequence of interest, which within or present within, the cell produces nucleic acid product which is independent or only partially dependent on the host system. The cassette or nucleic acid construct may be characterized as a promoter-independent non-naturally occurring, and in one embodiment comprises double-stranded and single-stranded nucleic acid regions. This construct contains a region in which a portion of the opposite strands are not
 15 substantially complementary, e.g., a bubble (even comprising at least one polyT sequence), or loop, or the construct comprises at least one single-stranded region. The construct is composed of naturally occurring nucleotides or chemically modified nucleotides or a synthetic polymer in part or a combination thereof. These structures are designed to provide binding of polymerizing enzymes or primers and the modifications provide for nuclease resistance or facilitate uptake by the target cell.

20 Referring to the constructs (A-F) depicted in Figure 3, the single stranded regions described in the constructs will contain coding sequences for nucleic acid primers present in the cell to facilitate initiation points of DNA polymerase in said cell. In the case of RNA polymerase, these constructs constitute promoter independent binding and initiation of RNA polymerase reaction. These constructs can be used *in vitro* and *in vivo* for production of nucleic acids. The position of the single stranded region adjacent to the double
 25 stranded specific sequence would provide a specific and consistent transcription of these specific sequences, both *in vitro* and *in vivo* independent of promoter. The replication (DNA) or transcription (RNA) products of these constructs can be single stranded nucleic acid which could have a sense or antisense function or could be double stranded nucleic acid.

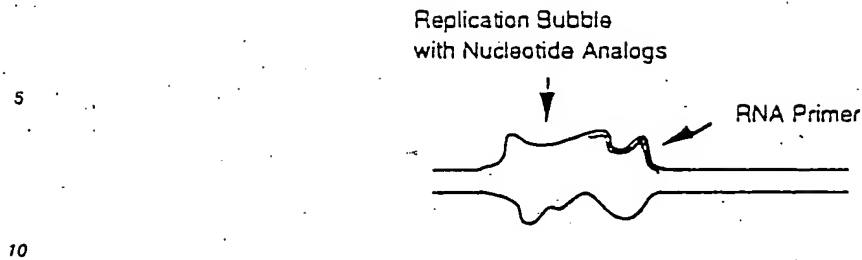
In Figure 13(A), a large bubble is located in the construct. In Figure 13(B), the two strands are
 30 noncomplementary at their ends, and thus do not form a bubble. In Figure 13(C), a double bubble is formed due to noncomplementarity at both ends. In Figure 13(D), a single-stranded region is shown in the middle of the construct leading to a partially single-stranded region (and no bubble formation). Figure 13(E) depicts a bubble at one end of the construct (compare with the two bubbles in the construct shown in Figure 13(C)). In Figure 13(F), a single bubble in the middle of the construct is shown. It should be readily appreciated by
 35 those skilled in this art that the above-depicted embodiments are representative embodiments not intended to be limiting, particularly in light of the present disclosure.

In vivo these constructs, with a specific primer present in the cell can initiate nucleic acid synthesis. When these primers are RNA, after initiation of nucleic acid synthesis, they can be removed by the action of ribonuclease H, thus vacating the primer binding sequence and allowing other primer molecules to bind
 40 and reinitiate synthesis. The cellular nucleic acid synthesizing enzymes can use these constructs to produce copies of a specific nucleic acid from the construct. Shown in Figure 14 (A-F) are corresponding illustrations of the constructs in Figure 13 (A-F), except that the production arrows (points and directions) are indicated.

These constructs could contain more than one specific nucleic acid sequence which in turn could
 45 produce more than one copy of each specific nucleic acid sequence. If two independent nucleic acid products are complementary, then they could hybridize and form multiple copies of a new double stranded construct that could have the properties of the novel construct. Furthermore they could contain promoter sites such as the host promoter therefore serving as an independent nucleic acid production source (the progeny).

50

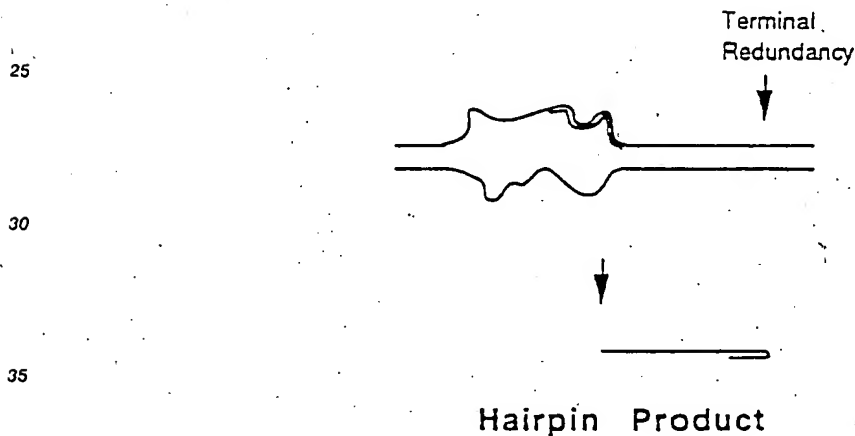
55



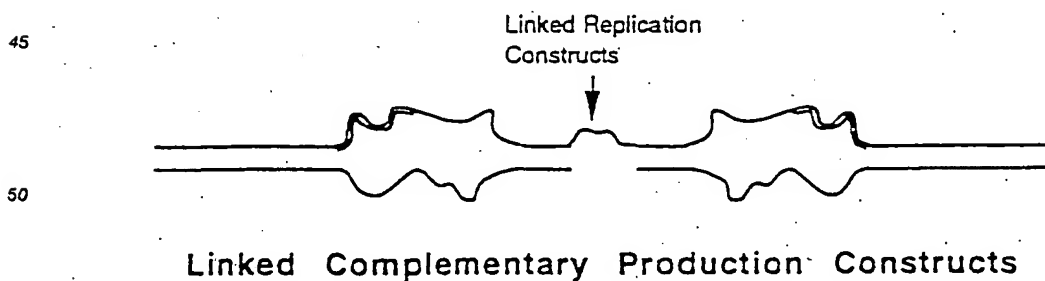
Primer-Dependent DNA Production Using Nucleic Acid Construct

15 The replication of this structure could result in the production of one strand of DNA product. Several alternative events may occur allowing for the formation of a second complementary strand. For example, a terminal loop could be inserted at the end of the construct such that the single stranded product will code for the synthesis of the complementary strand using the repair enzyme. Constructs can be made that produce single stranded DNA product that has a hairpin loop and therefore, can be used to form a double-

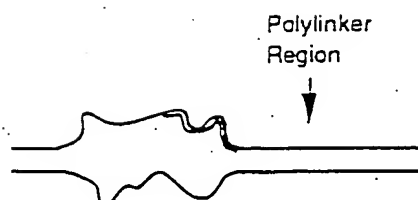
20 stranded product. Alternatively, constructs can be formed that produce nucleic acid in both polarity.



40 An alternative approach to the production of double stranded product is to covalently link two constructs that make complementary DNA strands.



55 The construct can be made to contain a poly linker region into which any sequence can be cloned. The result will be a transient accumulation of expressing genes within the cell to deliver sense, antisense or protein or any other gene product into the target cell.



Cloning Site in Production Constructs

Other processes within the invention herein described apply to the production of more than one copy of functional genes or antisense DNA or RNA in target cells.

Production of Primers

Primers can be produced by several methods. Single-stranded oligonucleotides in the range from between from about 5 to about 100 bases long, and preferably between from about 10 to about 40, and more preferably, between from about 8 to about 20 nucleotides. These ranges may further vary with optimally between from about 13 to about 30 for bacterial nucleic acid, and optimally between from about 17 to about 35 for eukaryote nucleotides would appear to be appropriate for most applications although it may be desirable in some or numerous instances to vary the length of the primers. Oligonucleotide primers can be most conveniently produced by automated chemical methods. In this way modified bases can be introduced. Manual methods can be used and may in some cases be used in combination with automated methods. All of these methods and automation are known and available in the art.

In addition nucleic acid primers can be produced readily by the action of T7 RNA polymerase, T3 polymerase, SP6 polymerase or any appropriate DNA or RNA polymerase on DNA templates or RNA templates containing the primer sequences extended from the corresponding RNA polymerase promoter sites or other nucleic acid synthesis start signals.

Detection of Products

DNA produced by the invention described herein can be detected by a variety of hybridization methods using homogeneous or non-homogeneous assays. DNA produced in tissues or cells, i.e., *in situ*, can be detected by any of the practiced methods for *in situ* hybridization. These include, but are not limited to, hybridization of the produced DNA with a nucleic acid probe labeled with a suitable chemical moiety, such as biotin. Probes used for the detection of produced DNA can be labeled with a variety of chemical moieties other than biotin. These include but are not limited to fluorescein, dinitrophenol, ethidium (see, for example, the disclosures of U.S. Patent Nos. 4,711,955; 5,241,060; and 4,707,440, *supra*).

The hybridized, labeled nucleic acid probe can be detected by a variety of means. These include but are not limited to reaction with complexes composed of biotin binding proteins, such as avidin or streptavidin, and color generating enzymes, such as horseradish peroxidase or alkaline phosphatase, which, in the presence of appropriate substrates and chromogens, yield colored products.

In accordance with this invention, DNA production from target sequences generally requires nucleic acid precursors, e.g., adenosine triphosphate, guanosine triphosphate, thymidine triphosphate and cytosine triphosphate, present in sufficient quantity and concentration in the reaction mixture. In other applications it may be advantageous to substitute one or more of the natural precursors with modified nucleotides. For example, when the invention described herein is being applied to the detection of specific nucleic acid sequences, immobilization of the produced DNA may be desirable. In such an instance, substitution of one or more of the natural nucleotide triphosphate precursors with a modified nucleotide, e.g., biotinylated deoxyuridine triphosphate, in place of thymidine triphosphate, would yield biotin-labeled DNA. The produced DNA could be separated by its affinity for a biotin binding protein, such as avidin, streptavidin or an anti-biotin antibody. A variety of nucleoside triphosphate precursors (U.S. Patent Nos. 4,711,955; 5,241,060; and 4,707,440, *supra*) labeled with chemical moieties which include, but are not limited to, dinitrophenol and fluorescein, and which can be bound by corresponding antibodies or by other binding proteins can be used in this manner. In other aspects of the invention, the produced DNA can be isotopically labeled by the inclusion of isotopically labeled deoxynucleotide precursors in the reaction mixture.

Labeled DNA, produced by the invention described herein, can function as probe nucleic acid to be used to detect specific target nucleic acid sequences.

In certain detection formats the primers may be removed from the reaction mixture by capturing the product through direct capture (Brakel et al., U.S. Patent Application Serial No. 07/998,660, filed on December 23, 1992, the contents of which have been disclosed in European Patent Application 0 435 150 A2, published on July 3, 1991; and the contents of which are also incorporated by reference herein), or sandwich capture. (Engelhardt and Rabbani, allowed U.S. Patent Application Serial No. 07/968,706, *supra*), or by modifying the primers at the 3' end with biotin or imminobiotin without an arm or a very short arm such that the avidin will recognize only the unincorporated primers (single stranded form) but not the incorporated due to the double stranded form and the short length of the arm. Additionally, the primer may be labeled with ethidium or other intercalating moiety. In this condition, the ethidium or other intercalating moiety may be inactivated (Stavrianopoulos, U.S. Patent Application Serial No. 07/633,730, filed on December 24, 1990, published as European Patent Application Publication No. 0 492 570 A1 on July 1, 1992; the contents of which are incorporated by reference) in the unhybridized oligo and not in the hybridized oligo:target.

Another aspect of this invention herein described is to provide for a conjugate of a nucleic acid polymerizing enzyme (RNA polymerase) with a nucleic acid construct said nucleic acid construct contains an initiation site such as a promotor site for the corresponding RNA polymerase which is capable of producing nucleic acid both *in vivo* and *in vitro*. The enzyme could be linked directly to the nucleic acid or through a linkage group substantially not interfering with its function or the enzyme could be linked to the nucleic acid indirectly by a nucleic acid bridge or haptene receptor where the enzyme is biotinylated and the nucleic acid construct contains an avidin or *vice versa* or when the nucleic acid construct contains sequences for binding proteins such as a repressor and an enzyme linked to said nucleic acid binding protein (U.S. Patent No. 5,241,060, *supra*, and Pergolizzi, Stavrianopoulos, Rabbani, Engelhardt, Kline and Olsiewski, U.S. Patent Application Serial No. 08/032,769, filed on March 16, 1993, published as European Patent Application Publication No. 0 128 332 A1 on December 19, 1984, the latter having been "allowed" by the European Patent Office, and further incorporated by reference herein).

Further in regard to the just-described conjugate of the present invention, the protein in one aspect comprises an RNA polymerase or a subunit thereof and the nucleic acid construct contains the corresponding RNA polymerase promoter. The RNA polymerase can be selected from T7, T3 and SP6, or a combination of any of the foregoing. In another embodiment, the protein in the conjugate comprises DNA polymerase or reverse transcriptase and the nucleic acid construct contains at least one sequence complementary to an RNA molecule. The construct can take the form of double-stranded, single-stranded, or even partially single-stranded. Further, the nucleic acid construct in the conjugate may comprise at least one chemically modified nucleotide or nucleotide analog. The linkages of the protein to the construct are described in the preceding paragraph. The nucleic acid produced by or from this conjugate comprises deoxyribonucleic acid, ribonucleic acid, or combinations thereof, or it may be antisense or sense, or both.

As described in the summary of the invention, the above-described conjugate may be utilized in an *in vivo* process for producing a specific nucleic acid. In other aspects of this *in vivo* process, the construct is further characterized as comprising (independently) at least one promoter, at least one complementary sequence to a primer present in the cell, or codes for the protein in the conjugate, or for a protein other than the protein in the conjugate. The other protein may comprise a nucleic acid polymerase. In the instant where the polymerase comprises an RNA polymerase, the nucleic acid construct may comprise a promoter for the RNA polymerase. Further, the polymerase can be a DNA polymerase or reverse transcriptase.

(a) Direct Attachment of a Polymerase to the Construct

For example, if a construct containing a RNA polymerase linked directly or indirectly to a DNA construct or cassette is introduced into a cell, the RNA polymerase will transcribe the nucleic acid in the construct and is completely independent of any host RNA polymerases. Each molecule introduced into a cell will produce multiple copies of a segment of the construct. In the first iteration, the attached polymerase can produce the RNA for the target sequence itself. (See Figure 3 (A)). Alternatively, the promoter, specific for the attached polymerase, may be linked to two separate sequences, namely the polymerase gene and the target gene. See Figure 3 (B). In this instance, the amount of polymerase initiating at the promoter site will increase as the polymerase gene is transcribed and translated. Finally, the coding sequence transcribed by the T₇ promoter (or any specific first promoter) may produce any RNA polymerase (including T₇ polymerase or polymerase III or others), and this polymerase may transcribe off of another or second promoter (or off of a different strength T₇ or other first promoter) to produce the transcript of the target

sequence. (See Figure 3 (C)).

Referring to the constructs or cassettes shown in Figure 4 (A-C), these can be derived by using standard recombinant DNA techniques. The appropriate piece of DNA can be isolated and covalently attached to the RNA polymerase under conditions whereby the RNA polymerase functions after being covalently attached to a solid matrix (Cook, P.R and Grove, F. Nuc. Acids Res, 20:3591-3598 (1992)). Methods of modifying the ends of DNA molecules for attachment of chemical moieties are well known (see, for example, U.S. Patent Application Serial No. 08/032,769, *supra*). The transcribed product can act per se as sense or antisense RNA or it can be translated into protein. The enzyme and/or nucleic acid constructs could be modified to facilitate transport and/or achieve resistance to degrading enzymes (U.S. Patent No. 5,241,060, *supra*).

(b) *In vivo* Amplification of Transcription

Constructs can be made that are dependent upon transcription or replication using a host polymerase. When such a construct contains a double promotor, the second promotor can be different than the first promotor or it can be a stronger or weaker version of the first promotor. Vectors can be chosen such that the constructs can either integrate into the chromosome, replicate autosomally or be replication-deficient and function only for transient expression. They can function in the nucleus or the cytoplasm if the target cell is eukaryotic. The figure below depicts various constructs or cassettes and is not limiting as to the possible variations contemplated by the present invention.

Referring to Figure 4 (A), the nucleic acid construct or cassette depicted in this figure contains a promotor that codes for the production of a polymerase that is not endogenous to the target cell. For example, an SV40 or RNA polymerase III promotor that codes for a T₇ RNA polymerase. Transcription and translation of these transcripts by cellular machinery results in the production of active T₇ RNA polymerase which will utilize the T₇ promotor to transcribe the target sequence (Fuerst, T.R. et al., Proc Nat Acad Sci USA 83:8122 (1986)) have shown high levels of transient expression using a dual construct system with the T₇ RNA polymerase gene on one construct and the target gene behind the T₇ promotor on the other construct. The simplest iteration of this construct is that the genes coding for the polymerase code for a polymerase that exists within the cell and therefore is not recognized by the host organism as a foreign protein and does not induce an immune response.

In Figure 4 (B), an additional autocatalytic cycle has been added whereby the extent of transcription of the target gene is enhanced by the production of T₇ RNA polymerase throughout the transient expression cycle.

In Figure 4 (C), the construct or cassette is similar to Figure 4 (B) with the additional element that there is a down regulation of the autocatalytic cascade by competition by a high efficiency promotor with a low efficiency transcriptional promotor.

Three Constructs with Promoters for Endogenous RNA Polymerase

As described in the summary, the present invention further provides a construct comprising a host promoter located on the construct such that the host transcribes a sequence in the construct coding for a different RNA polymerase which after translation is capable of recognizing its cognate promoter and transcribing from a DNA sequence of interest in the construct with the cognate promoter oriented such that it does not promote transcription from the construct of the different RNA polymerase. In one feature of this construct, the host promoter comprises a prokaryotic promoter, e.g., RNA polymerase, or eukaryotic promoter, e.g., Pol I, Pol II, Pol III, or combinations thereof, such prokaryotic or eukaryotic promoter being located upstream from the host promoter. The second RNA polymerase may be selected from various members, including T₇, T₃ and SP6, or combinations thereof. The DNA sequence of interest may comprise sense or antisense, or both, or it may comprise DNA or RNA, or still yet, it may encode a protein. The construct may further comprise at least one chemically modified nucleotide.

Additionally, promoters that will be read by polymerases within the target cell can be linked to the production of additional polymerase specific for that promotor or other promoters. The polymerases can be for example, T₇ polymerase, RNA polymerase III, or any other polymerase. A second promoter keyed sequence can be in the construct such that a second polynucleotide can be synthesized from the construct. It can code for the production of antisense or sense RNA or DNA molecules. These constructs or cassettes can be created using standard recombinant DNA techniques.

The property and structure of all nucleic acid constructs provided in accordance with this invention is applicable to each other in combination, *in toto* or in part. That is to say, in the conjugate comprising a

protein and a nucleic acid construct, the construct could include, for example, chemical modification and bubble structure or single-stranded regions for primer binding sites or RNA initiation sites. Other variations would be recognized by those skilled in the art in light of the detailed description of this invention.

One subject matter of the present invention is process A which is an *in vitro* process for producing more than one copy of a specific nucleic acid, said process being independent of a requirement for the introduction of an intermediate structure for the production of said specific nucleic acid, said process comprising the steps of:

- (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
- 10 (b) contacting said sample with a mixture comprising:
 - (i) nucleic acid precursors,
 - (ii) one or more specific nucleic acid primers each of which is complementary to a distinct sequence of said specific nucleic acid, and
 - (iii) an effective amount of a nucleic acid producing catalyst; and
- 15 (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing more than one copy of said specific nucleic acid.

Specific embodiments of this process A are the following items:

1. The process A wherein said specific nucleic acid is single-stranded or double-stranded.
2. The process A wherein said specific nucleic acid is selected from deoxyribonucleic acid, ribonucleic acid, a DNA:RNA hybrid or a polymer capable of acting as a template for a nucleic acid polymerizing catalyst.
3. The process A wherein said specific nucleic acid is in solution.
4. The process of item 3 further comprising the step of treating said specific nucleic acid with a blunt-end promoting restriction enzyme.
- 25 5. The process A wherein said specific nucleic acid is isolated or purified prior to the contacting step (b) or the reacting step (c).
6. The process of item 5 wherein said isolation or purification of said specific nucleic acid is carried out by means of sandwich or sandwich capture.
7. The process of item 6 further comprising the step of releasing said captured specific nucleic acid.
- 30 8. The process of item 7 wherein said releasing step is carried out by means of a restriction enzyme.
9. The process A wherein said nucleic acid precursors are selected from nucleoside triphosphates and nucleoside trisphosphate analogs, or a combination thereof.
10. The process of item 9 wherein said nucleoside triphosphates are selected from deoxyadenosine 5'-triphosphate, deoxyguanosine 5'-triphosphate, deoxythymidine 5'-triphosphate, deoxycytidine 5'-triphosphate, adenosine 5'-triphosphate, guanosine 5'-triphosphate, uridine 5'-triphosphate and cytidine 35 5'-triphosphate, or a combination of any of the foregoing.
11. The process of item 9 wherein said nucleoside triphosphate analogs are naturally occurring or synthetic, or a combination thereof.
12. The process of item 9 wherein at least one of said nucleoside triphosphates or nucleoside triphosphate analogs is modified on the sugar, phosphate or base.
- 40 13. The process A wherein said specific nucleic acid primers are selected from deoxyribonucleic acid, ribonucleic acid, a DNA:RNA copolymer, or a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization.
14. The process A wherein said specific nucleic acid primers comprise oligo- or polynucleotides.
- 45 15. The process A wherein said specific nucleic acid primers contain a 3'-hydroxyl group or an isosteric configuration of heteroatoms.
16. The process of item 15 wherein said heteroatoms are selected from nitrogen, sulfur, or both.
17. The process A wherein said specific nucleic acid primers are not substantially complementary to one another.
- 50 18. The process of item 17 wherein said specific nucleic acid primers contain no more than five complementary base-pairs in the sequences therein.
19. The process A wherein said specific nucleic acid primers comprise from about 5 to about 100 nucleotides.
20. The process of item 19 wherein said specific nucleic acid primers comprise from about 8 to about 20 nucleotides.
- 55 21. The process A wherein said specific nucleic acid primers comprise at least one non-complementary nucleotide or nucleotide analog base, or at least one sequence thereof.

22. The process of item 21 wherein said specific nucleic acid primers further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.
23. The process of item 22 wherein said noncomplementary nucleotide or nucleotide analogs in said specific nucleic acid primers comprise from about 5 to about 20 nucleotides.
- 5 24. The process of item 21 wherein said noncomplementary base sequence or sequences are linked together by other than a phosphodiester bond.
25. The process A wherein said nucleic acid producing catalyst is selected from DNA polymerase and reverse transcriptase, or both.
26. The process A wherein said nucleic precursors or said specific primers or both are modified by at least one intercalating agent.
- 10 27. The process A further comprising the step (d) of detecting the product produced in step (c).
28. The process of item 27 wherein said detecting step (d) is carried out by means of incorporating into the product a labeled primer, a labeled precursor, or a combination thereof.
29. The process A further comprising the step of regenerating said one or more specific nucleic acid primers.
- 15

Another subject matter of the invention is process B which is an *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:

- (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
- 20 (b) contacting said sample with a mixture comprising:
- (i) nucleic acid precursors,
- (ii) one or more specific polynucleotide primers comprising at least one ribonucleic acid segment each of which primer is substantially complementary to a distinct sequence of said specific nucleic acid, and
- 25 (iii) an effective amount of a nucleic acid producing catalyst; and
- (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and
- (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.
- 30

Specific embodiments of this process B are the following items:

1. The process B wherein said step (d) removing is carried by digestion with an enzyme.
2. The process of item 1 wherein said enzyme comprises ribonuclease H.
- 35 3. The process B wherein said nucleic acid precursors are modified or unmodified.
4. The process B wherein said specific polynucleotide primers further comprise deoxyribonucleic acid.
5. The process B wherein said specific polynucleotide primers contain a 3'-hydroxyl group or an isosteric configuration of heteroatoms.
6. The process of item 5 wherein said heteroatoms are selected from nitrogen, sulfur, or both.
- 40 7. The process B wherein said specific polynucleotide primers further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.

A further subject matter of the present invention is process C which is an *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:

- 45 (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
- (b) contacting said sample with a mixture comprising:
- (i) unmodified nucleic acid precursors,
- (ii) one or more specific chemically-modified primers each of which primer is substantially complementary to a distinct sequence of said specific nucleic acid, and
- 50 (iii) an effective amount of a nucleic acid producing catalyst; and
- (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and
- (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.
- 55

Specific embodiments of process C are the following items:

1. The process C wherein said step (d) removing is carried by digestion with an enzyme.

2. The process of item 1 wherein said enzyme comprises ribonuclease H.

3. The process C wherein said specific chemically modified primers are selected from ribonucleic acid, deoxyribonucleic acid, a DNA:RNA copolymer, and a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization, or a combination of any of the foregoing.

4. The process C wherein said specific chemically modified primers contain a 3'-hydroxyl group or an isosteric configuration of heteroatoms.

5. The process of item 4 wherein said heteroatoms are selected from nitrogen, sulfur, or both.

6. The process C wherein said specific chemically modified primers are selected from nucleoside triphosphates and nucleoside triphosphate analogs, or a combination thereof, wherein at least one of said nucleoside triphosphates or analogs is modified on the sugar, phosphate or base.

7. The process C wherein said specific chemically modified primers further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.

Another embodiment of the invention is process D which is an *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:

(a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;

(b) contacting said sample with a mixture comprising:

(i) unmodified nucleic acid precursors,

(ii) one or more specific unmodified primers comprising at least one segment each of which primer comprises at least one non-complementary sequence to a distinct sequence of said specific nucleic acid, such that upon hybridization to said specific nucleic acid at least one loop structure is formed, and

(iii) an effective amount of a nucleic acid producing catalyst; and

(c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and

(d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.

Specific embodiments of process D are the following items:

1. The process D wherein said step (d) removing is carried by digestion with an enzyme.

2. The process of item 1 wherein said enzyme comprises ribonuclease H.

3. The process D wherein said specific unmodified primers are selected from ribonucleic acid, deoxyribonucleic acid, a DNA:RNA copolymer, and a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization, or a combination of any of the foregoing.

4. The process D wherein said specific unmodified primers further comprise from about 1 to about 200 noncomplementary nucleotide or nucleotide analogs.

Another embodiment of the invention is construct A which is a promoter-independent non-naturally occurring nucleic acid construct which when present in a cell produces a nucleic acid without the use of any gene product coded by said construct.

Specific embodiments of the construct A of the invention are the following items:

1. The construct A comprising double-stranded and single-stranded nucleic acid regions.

2. The construct A wherein said nucleic acid comprises deoxyribonucleic acid, ribonucleic acid, a DNA:RNA copolymer, or a polymer capable of hybridizing or forming a base-specific pairing complex and initiating nucleic acid polymerization.

3. The construct A comprising at least one modified nucleotide or nucleotide analog.

4. The construct A comprising at least one single-stranded region.

5. The construct of item 4 wherein said single-stranded region comprises a bubble.

6. The construct of item 5 wherein said bubble comprises at least one complementary sequence to a nucleic acid present in the cell.

7. The construct of item 5 wherein said bubble comprises at least one polyT sequence.

Another embodiment of the invention is a conjugate which is a conjugate comprising a protein-nucleic acid construct, said nucleic acid construct not coding for said protein, and which conjugate produces a nucleic acid when present in a cell.

Specific embodiments of the conjugate of the invention are the following items:

1. The conjugate wherein said protein comprises an RNA polymerase or a subunit thereof and the nucleic acid construct contains the corresponding RNA polymerase promoter.
2. The conjugate of item 1 wherein said RNA polymerase is selected from T7, T3 and SP6, or a combination of any of the foregoing.
- 5 3. The conjugate wherein said protein comprises DNA polymerase or reverse transcriptase and said nucleic acid construct contains at least one sequence complementary to an RNA molecule.
4. The conjugate wherein said nucleic acid construct is double-stranded, single-stranded, or partially single-stranded.
- 10 5. The conjugate wherein said nucleic acid construct comprises at least one chemically modified nucleotide or nucleotide analog.
6. The conjugate wherein said protein is linked to said nucleic acid construct by means of a covalent linkage.
7. The conjugate wherein said protein is linked to said nucleic acid construct by means of base-pairing of complementary nucleic acid sequences.
- 15 8. The conjugate wherein said protein is linked to said nucleic acid construct by means of a nucleic acid binding protein.
9. The conjugate of item 8 wherein said nucleic acid binding protein comprises a repressor protein bound to an enzyme.
10. The conjugate wherein said protein is linked to said nucleic acid construct by means of ligand receptor binding.
- 20 11. The conjugate wherein the nucleic acid produced is deoxyribonucleic acid, ribonucleic acid, or a combination thereof.
12. The conjugate wherein the nucleic acid produced is sense or antisense, or both.

A further embodiment of the invention is process E which is an *in vivo* process for producing a specific nucleic acid, said process comprising the steps of:

- (a) providing a conjugate comprising a protein-nucleic acid construct, said conjugate being capable of producing a nucleic acid when present in a cell; and
- (b) introducing said conjugate into a cell, thereby producing said specific nucleic acid.

Specific embodiments of process E are the following items:

- 30 1. The process E wherein said construct comprises at least one promoter.
2. The process E wherein said construct comprises at least one complementary sequence to a primer present in the cell.
3. The process E wherein said nucleic acid construct codes for the protein in said conjugate.
4. The process E wherein said nucleic acid construct codes for a protein other than the protein in said conjugate.
- 35 5. The process of item 4 wherein said other protein comprises a nucleic acid polymerase.
6. The process of item 5 wherein said polymerase comprises an RNA polymerase and said nucleic acid construct comprises a promoter for said RNA polymerase.
7. The process of item 5 wherein said polymerase comprises a DNA polymerase or reverse transcriptase.
- 40

A further embodiment of the invention is construct B which is a construct comprising a host promoter located on the construct such that the host transcribes a sequence in the construct coding for a different RNA polymerase which after translation is capable of recognizing its cognate promoter and transcribing from a DNA sequence of interest in the construct with said cognate promoter oriented such that it does not promote transcription from the construct of said different RNA polymerase.

Specific embodiments of the construct B of the invention are the following items:

1. The construct B wherein said host promoter comprises a prokaryotic or eukaryotic promoter upstream from the host promoter.
2. The construct B wherein said host promoter and the promoter for the second RNA polymerase are located on opposite strands.
3. The construct of item 1 wherein said prokaryotic promoter comprises a RNA polymerase.
4. The construct of item 1 wherein said eukaryotic promoter is selected from Pol I, Pol II and Pol III, or a combination of any of the foregoing.
5. The construct B wherein said second RNA polymerase is selected from T7, T3 and SP6, or a combination of any of the foregoing.
- 55 6. The construct B wherein said DNA sequence of interest comprises sense or antisense, or both.
7. The construct B wherein said DNA sequence of interest comprises deoxyribonucleic acid or ribonucleic acid.

8. The construct B wherein said DNA sequence of interest encodes a protein.

9. The construct B comprising at least one chemically modified nucleotide.

The examples which follow are set forth to illustrate various aspects of the present invention but are not intended to limit in any way the scope as more particularly set forth in the claims below.

5

EXAMPLES

Example 1

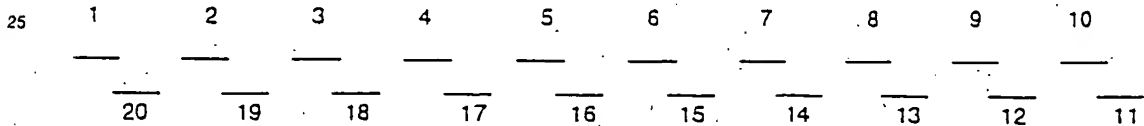
10 Primers

A set of twenty single stranded oligonucleotide primers, fifteen nucleotides long, were chemically synthesized.

The first set of 10 primers was complementary to one strand of M13mp18 replicative form (RF) starting at base 650 and extending to base 341. An interval of 15 nucleotides separated successive primers. The second set of 10 primers contained sequences identical to the single-stranded M13mp18 phage genome starting at base 351 and extending to base 635, again with 15 nucleotide gaps separating successive primers. There is a complementarity of 5 bases between opposing primers, but at an ionic concentration of 0.08M NaCl and 45°C these primers will not hybridize to each other. The sequences of the primers are shown in Figure 6.

20

ARRANGEMENT OF OLIGONUCLEOTIDE PRIMERS IN AMPLIFICATION REACTION



30

Primer 1 begins at base 650 and primer 11 begins at base 351.

Example 2

35 Amplification Target

The target of amplification was the M13mp18 RF. This was digested with either *TaqI* or a combination of *Bam*H1 and *Eco*R1. *Eco*R1 and *Bam*H1 cut at sites close to each other and digestion with either enzyme alone would transform the circular RF molecule into a linear DNA molecule. The *TaqI* enzyme digests M13mp18 RF yielding 12 fragments. The sequence to be amplified (nucleotides 351 to 650) was flanked in the *Bam*H1/*Eco*R1 digested RF by two regions, 1,371 bases and 5,601 bases, and *TaqI*-digested M13mp18 RF was flanked by regions of 15 and 477 nucleotides (see Figure 7).

In amplification experiments, the restriction digests were used without any further purification. For amplification, a control of irrelevant DNA (calf thymus) was employed.

45 The precursors were added in 50μl aliquots. One 10μl aliquot of the precursors was mixed with 90μl H₂O and loaded on a glass fiber filter, dried and counted. The counts were multiplied by 5 and divided by 160 (nmoles in the incubation mix). Specific activity is the cpm/nmoles of nucleotides.

Amplification is measured as follows. The total counts are determined and this number is divided by the specific activity of the precursors to determine the number of nanomoles of incorporation. The target (in n grams) is divided by 330 (average molecular weight of nucleotide) to determine the nanomoles of input target phosphate. The amplification is then calculated by dividing the nanomoles of product by the nanomoles of input target.

55

Example 3The Effect of Primer Concentration on the Amplification of Target DNA.

5 An incubation mixture of 130 μ l contained the following reaction components: 40 mM sodium phosphate, pH 7.5, 400 μ M each of the four deoxynucleotide triphosphates, 5 mM dithiothreitol, 40 ng of Taq1-digested M13mp18 RF (containing 3.5 ng of the Taq1 fragment to be amplified), and all 20 primers (at 0.04 OD/ml, 0.4 OD/ml or 0.8 OD/ml) and 15 units of Klenow fragment of DNA polymerase. The mixture was left at room temperature for 20 minutes in order to allow the enzyme to cover all of the initiation sites on the template. The polymerization was then initiated by the addition of Mg^{++} , 7 mM final concentration, and the tubes were placed in a 45°C bath. After 1 hour an additional 15 units of the enzyme were added, and the incubation was continued for another hour. The reaction was stopped with 100 μ moles of EDTA, 100 μ g sonicated calf thymus DNA were added, and the nucleic acids were precipitated with 1.0 ml of cold 10% TCA for 60 minutes at 0°C. The mixture was filtered through a glass fiber filter, the filter was washed 3 times with cold 5% TCA, then twice with ethanol, dried and counted in a Beckman liquid scintillation counter.

The specific activity of the nucleotide precursors was 9,687 cpm/nmole. The tagged Taq1 DNA fragment contained 0.0106 nmoles of nucleotides.

Primer Concentration	Incorporation (cpm)	Incorporation (nmoles nucleotide)	Amplification
0.04 OD/ml	32,482	3.35	316
0.4 OD/ml	366,260	37.8	3566
0.8 OD/ml	512,260	52.88	4988

Example 4The Random Priming Activity of the Primers on Calf Thymus DNA.

To test for the effect of the primers on the background, an assay was performed, as described in the preceding example (Example 3 above), in which background was determined with and without primers as well as with and without melting of the calf thymus DNA.

The amplification conditions were the same as in Example 1 except that only 5 μ g (15.0 nmoles) calf thymus DNA were used as a target. The DNA employed was double stranded or heated at 100°C for 10 minutes in the presence or absence of primers (0.4 OD/ml each) before being chilled on ice.

Double Stranded DNA	Melted DNA	Primers	Incorporation cpm	Incorporation umoles	Amplification
+			239,100	24.68	1.64
+		+	276,540	28.54	1.90
	+	+	556,560	57.45	3.83
	+		28,432	2.93	0.19

This experiment suggests that the random priming activity of the primers is not substantial, that incorporation on double stranded DNA is due to the nicks on the DNA molecules, and that melting abolishes to a large extent the priming positions on the irrelevant DNA.

Example 5Amplification of the M13 Fragment in the presence of a large Excess (1500-Fold) of Irrelevant DNA

The amplification conditions were the same as in Example 1. Primers (0.4 OD/ml), 5 μ g calf thymus DNA and 40 ng M13mp18 DNA containing 3.5 ng of fragment were employed in this example.

Calf Thymus DNA	M13mp18 DNA	Incorporation cpm	Incorporation nmoles	Amplification
+		575,440	59.4	3.96x
	+	338,900	35.0	3,300x
+	+	713,440	73.6	

The experimental results above show that the target can be amplified in the presence of large amounts of irrelevant DNA. The net amplification was 1,343 even though in this case the target DNA inhibits the amplification of the irrelevant DNA by competing for initiation points. It is possible that the amplification was even larger.

These experimental results were also analyzed by running the samples on a 2% agarose gel. In Figure 8 it can be seen that the calf thymus template (lane 3) only gives high molecular weight DNA bands composed of a mixture of input DNA as well as DNA synthesized by random priming (as seen in the incorporation figures in the Table above given for this example). On the other hand, it can be seen that the mp18 template (lane 2) gives a distinct pattern of lower molecular weight bands, and in lane 1, similar bands are observed when the mp18 template was mixed with 1500 times as much calf thymus DNA demonstrating that the foreign DNA did not significantly affect the amplification of DNA from the mp18 template.

Example 6

Amplification of Different Restriction Digests

The incubation conditions were the same as in Example 4. Forty nanograms of total M13mp18 DNA were used in each experiment with 0.4 OD/ml primers. In one case, the M13mp18 DNA was cut in only one position (using *EcoR1*) leaving the fragment to be amplified flanked by two large pieces. In the other case where the RF was treated with *Taq1*, the fragment was contained in one 639 base pair fragment. The specific activity of the precursors was 8.385 cpm/nmole.

	Incorporation cpm	Incorporation nmoles
Large Fragment	393,480	46.92
Small Fragment	262,808	31.34

These experimental results show that the enzyme does not extend polymerization very far from the region where the primers hybridize, otherwise a much larger incorporation using the large piece would have been otherwise expected because the elongation of the primers by the enzyme can extend in both directions.

Example 7

A Comparison of Synchronized and Unsynchronized Reactions

In all of the preceding experiments, the enzyme was preincubated with the target-primer mixture to allow binding of the enzyme at the 3' end of the hybridized primers on the target, followed by the addition of magnesium to initiate polymerization. The conditions were the same as in Example 1.

To assay the effect of this synchronization on the extent of the reaction, the incorporation in a synchronized reaction was compared to an unsynchronized reaction initiated by adding magnesium to the complete reaction mix before enzyme addition. The reaction conditions are described in Example 3. The specific activity was 9687 cpm/nmole.

	Incorporation cpm	Incorporation nmoles	Amplification
Synchronized	495,080	51.1	4818
Unsynchronized	416,380	42.9	4052

The results above demonstrate that synchronization of the reaction is not essential for the amplification reaction.

Example 8

The Effect of Variations of the Reaction Conditions on the Product Produced by the Procedure of Example 3

A reaction was performed according to the reaction conditions of Example 3 in which twenty primers were added to the reaction mixture as well as the *Taq* 1 fragments (40 nanograms, i.e., 3.5 nanograms of insert that will hybridize with the primers) described in Example 3 with the exception that the buffer was altered. In the first lane of the gel shown in Figure 9, the reaction was performed without target DNA added. In lane 2 the reaction was performed in a phosphate buffer (0.04 M, pH 7.5). Lane 3 contains the molecular weight buffers of *Msp* I digestion of pBR322 DNA. In the fourth lane the reaction was performed in which the phosphate buffer was substituted by MOPS buffer at 0.1 M and pH 7.5 (measured 25 °C). It can be seen that the reaction in the phosphate buffer produced an agglomeration of DNAs that when dissociated by heat or other double helix disrupting agents lead to a number of products of a size smaller than the agglomeration structures. The size distribution of the products in the MOPS-buffered reaction corresponds to the distances between certain of the oligo primer binding sites. The smallest is approximately 76 nucleotide pairs in size which is approximately the distance between the closest specific oligo primer binding sites.

Example 9

Effect of Various Buffers on the Amplification Reaction.

The buffer used for the amplification reaction can have significant effects upon the degree of amplification. In the following example, phosphate buffer (which was employed in Example 7) was compared with the following zwitterion buffers:

- 4-morpholinoethyl sulfonate (MES),
- 4-morpholinopropionyl sulfonate (MOPS),
- N-dimethylaminobutyric acid (DMAB), and
- N-dimethylglycine (DMG).

Trizma base was used to adjust MES or MOPS to pH 7.5, DMAB to pH 7.8, and DMG to pH 8.6. In the previous experiments, 4.0 ng of mp18 (containing 3.5 ng of the target fragment) was used as a template. In this experiment, the amount of template was reduced ten-fold compared to those experiments (4 ng of mp18; 350 pg of target fragment). Other changes in the experimental procedure was the omission of DTT and the use of a single addition of 10 units of Klenow polymerase. Mg^{++} and dNTP concentrations (7.5 mM and 400 μ M each dNTP) were as described previously.

As before, reactions were preincubated at room temperature for 30 minutes prior to the addition of the Mg^{++} . After addition of Mg^{++} , reactions were immediately transferred to a 45 °C water bath and incubated for 4 hours. The reaction was stopped by the addition of 5 μ l of 500 mM EDTA to give a final concentration of approximately 20 mM.

For evaluation of the extent of polymerization, an aliquot of 40 μ l (out of a 120 μ l incubation mix) was mixed with 50 μ g of sonicated calf thymus DNA and precipitated on ice with 1 ml of 10% TCA. After one hour, the precipitate was collected on glass fiber filters, washed 3 times with 5% of cold TCA, 2 times with 95% ETOH, dried and counted in a liquid scintillation counter. The input was measured by the addition of radioactive precursor onto a filter without precipitation with TCA and counted as before. The results are given in the table below. As controls, the reactions were also carried out without the addition of any target template.

Buffer	Incorporation From Template (in cpm)	No Template Control (in cpm)	Template-Specific Incorporation (in cpm)	Net Synthesis (nanomoles)	Amplification Factor
Phosphate	4,008	2,628	1,380	0.255	240
MES	299,367	212,778	86,589	16.03	15,123
MOPS	184,500	49,521	114,979	21.28	20,075
DMAB	207,239	5,859	211,380	39.13	36,915
DMG	182,655	32,012	150,643	27.89	26,311

Compared to the no template control, the highest efficiency of amplification was obtained with the DMAB buffer. The results of this experiment demonstrated that an amplification of the target region approaching 37,000 fold could be obtained. It should be noted that another buffer, MES, gave higher incorporation, but the no template control demonstrated that there was non-specific polymerization leading to a net amplification of only 20,000 fold. The next best buffer system was DMG where net amplification was over 26,000 fold, followed by MOPS with 20,000 fold amplification.

The results of this experiment were also analyzed qualitatively by ethanol precipitating the remaining 80 μ l of the reaction mixtures, resuspending them in 80 μ l of TE buffer and running 10 μ l aliquots on 2% agarose gels. These results are shown in Figure 10 and agree with the results shown in the table above.

Example 10

Incorporation of radioactive precursors measures total synthesis of DNA including both specific as well as template-independent DNA synthesis. Oligos No. 1,3,5,7,9,12,14,16,18 and 20 from Example 1 were employed in a series of amplification reactions. This limited number was chosen such that there would be a region within the amplicon that does not correspond to any of the primers, allowing the use of a 30 base probe (bases 469 to 498) labeled with biotin that corresponds to this open region.

The experimental design was to use DMAB and DMG buffers. Example 9 had previously shown little or no template-independent synthesis with DMAB and substantial template-independent synthesis with DMG. Reactions with and without Taq digested mp18 were carried out. The reaction mixtures were precipitated with ethanol, resuspended in TE buffer and aliquots were electrophoresed through a 2% agarose gel. A southern blot was made from this gel and probed with 200 ng/ml labeled oligo in 31% formamide/ 2X SSC at 25°C for 2 hours and washed 3 X with 0.1X SSC/0.1% Triton X-100 for 5 minutes each at 37°C. Membranes were developed using an alkaline phosphate detection system obtained from Enzo Biochem, Inc.

As seen in Figure 11, this set of experiments demonstrates that the product of the amplification is strongly dependent upon the specific buffer used in the reaction. The best results were obtained with DMAB buffer where essentially no incorporation (data not shown) or hybridization (Figure 11, lane 1) with the reaction mixture from the no template control sample. The template dependent synthesis with DMAB (Figure 11, lane 2) produced DNA that hybridized with the labeled probe.

The nature and origin of the non-template derived synthesis achieved with DMG buffer (Figure 11, lane 3) is still under current study.

Example 11

Determination of the Nature of the Ends of the Amplified Product

If the product strands act as the template for polymerization of nucleic acid then the products should have blunt ends. One method of assaying for the presence of blunt ends is based on the notion that these molecules will undergo blunt end ligation. Molecules with 'ragged' ends (single stranded tails on the 3' or 5' end) will not participate in the ligation reaction.

Because the amplified product is initiated using chemically synthesized primer molecules, the 5' ends will not under phosphorylation. The first step of this proof will be to phosphorylate the 5' ends of both single stranded and double stranded molecules. These 5' phosphorylated molecules will then be ligated using the

T4 DNA ligase. The unamplified DNA will act as the negative control and a PCR-generated amplicon will act as the positive control.

As can be seen in the gel reported in Figure 12, T4 ligase treatment increases the molecular weight of the amplified product selectively. This is most apparant in lane 4 of Figure 12, where there is an appreciable increase in size observed as a result of the completed ligation reaction.

The positive control with the PCR-generated amplicon (primed by oligos initiating at nucleotide 381 and from nucleotide 645 of the template which predicts an amplicon of 264 nucleotides) also show a shift in position after ligation (lane 7). Because there was not much DNA included in this reaction, the appearance of a spectrum of multimers of the amplicon was not observed, but the loss of material from the position of the unligated material (lanes 5 and 6) was noted. Some material left at the position of the untreated amplicon in lane 7 was also noted. It is possible that this material does not participate in the ligation reaction because of the addition of A to the 3' end of the amplicon which is a property of the Taq polymerase.

15 *Example 12*

Amplification from non-denatured template

To explain the high level of amplification in this system, it was assumed that some of the primers might be able to initiate DNA synthesis by inverting the ends of double-stranded DNA products synthesized during amplification. This "breathing" was demonstrated in the following experiment. The template was a blunt-ended double-stranded DNA molecule obtained from Dr. Christine L. Brakel, the blunt ends extending from bases 371 to 645 in the mp18 DNA sequence. These ends exactly match primers Nos. 1 and 12 (described in Example 1). In this experiment, no radioactive precursors were used. Analysis was performed by gel electrophoresis through 2% agarose. Reagent conditions were the same as Example 10 where DMG was used as the buffer, but only 2 primers, No. 1 and No. 2 were used and no denaturation of the starting template was performed. In Figure 13, for comparison purposes, the same amount of DNA was used as the input on the gel (lane 1). In lane 2, no template was added. In lane 3, the complete reaction mix is shown. In lane 4, 12 times as much DNA as the template input in either lanes 1 or 3 has been included as a size marker. In both lanes 2 and 3, some non-specific synthesis can be seen, but the specific copying of the template can clearly be distinguished in lane 3. Therefore, as lane 3 indicates, newly synthesized DNA of the same size as the input was formed using non-denatured double-stranded DNA, proving that the double-stranded blunt ends can serve as initiation points for replication.

35 *Example 13*

Amplification from RNA template

Although it has been demonstrated by the present invention that DNA can be amplified, it would be useful, however, to also be able to employ RNA as a potential template. Accordingly, the double-stranded DNA molecule used in Example 12 was ligated into the Sma I site of a vector pIB131 (obtained from International Biotechnology Corp) that contains a promotor for T7 RNA polymerase. Using standard methodologies, an RNA transcript was synthesized encompassing the same sequences used in example 12. This transcript was amplified using standard conditions with all 20 primers in DMG buffer. Taq digested mp18 DNA was used as a control. As seen in Figure 14 there was extensive synthesis. There are characteristic bands that appear in lane 4, the reaction with the RNA template, as well as in lane 2, the reaction with the DNA template that do not appear in the template independent synthesis seen in lanes 1 and 5.

This demonstrates that the system is capable of utilizing the RNA transcript as a template without the introduction of any other enzyme besides the Klenow, thus proving that the Klenow enzyme can be used as a reverse transcriptase as indicated in the disclosure. This result was studied further by making a Southern blot of the gel seen in Figure 14 and probing with nick-translated biotinylated mp18 DNA using a nick translation kit obtained from Enzo Biochem, Inc. As seen in Figure 15, there was little or no hybridization of the probe to the reaction product of the template independent reactions (lanes 1 and 5) whereas extensive hybridization was observed with the RNA derived reaction (lane 4) as well as the DNA template derived reaction (lane 2), as expected.

Example 14

Strand Displacement Using Ethidium-Labeled Oligonucleotides

5 Three oligonucleotides with the sequence listed in Figure 16 were prepared and labeled F1, F1C and F3. The unlabeled complement of F1C was hybridized to unlabeled F1. The ratio of F1C: F1 for the hybridization was 1:2. (F1C at a concentration of 0.13 O.D./ml and F1 at a concentration of 0.26 O.D./ml.) Hybridization was performed in 1X SSC for two hours at 45°C.

10 Aliquots of the hybrid were mixed with different amounts of ethidium-labeled F1 (F1E) in 1X SSC and incubated for 18 hours either at 43°C. or at 37°C. The ratios of F1E oligo to the unlabeled oligo F1C was 1:1, 2:1, 3:1 and 4:1. (The 1:1 reaction contained 0.0325 O.D. of the F1E, 0.065 O.D. of F1 and 0.0325 O.D. of F1C.) At the end of the incubation period, 50µl of each mixture was incubated with 50µl of diazonium mixture for 5 minutes at room temperature. To prepare the diazonium mixture, 10 µl of the diazonium stock solution, (50 mM in 1M HCl), was added to 100 µl of cold dilution buffer, (1 X SSC and 0.2 M KHCO₃, prepared fresh). The diazonium stock solution is stored at -20°C.

15 Under these conditions the diazonium will destroy the fluorescence associated with the ethidium in single stranded oligonucleotides. See, e.g., European Patent Application Publication No. 0 492 570 A1, published on July 1, 1992, based on priority document, U.S. Patent Application Serial No. 07/633,730, filed on December 24, 1990, the contents of which are incorporated by reference. But the diazonium will not destroy the fluorescence associated with the ethidium that has intercalated into the double stranded DNA. The survival of the ethidium, under these reaction conditions, is a measure of the extent of formation of a double helix by the ethidium-labeled oligonucleotides, thus indicating displacement of the non-ethidium containing strand by that of the ethidium labeled. This property of the ethidium labeled oligonucleotides by primers can be usefully employed to facilitate initiation of polymerization on double stranded templates. As
25 seen in the figure in Figure 17, the ethidium-labeled oligo displaces the non-ethidium-labeled oligo better at 43°C than at 37°C.

Example 15

30 T7 Promoter Oligonucleotide 50 Mer Labeled with Ethidium

An oligonucleotide 50-mer including the T7 promoter region of IBI 31 plasmid constructs (plasmid sequences derived from manufacturer, International Biotechnology, Inc.) was synthesized. Its sequence is as follows:

35
3'-TAC T*AA T*GC GGT* CT*A T*AG T*T-AA TCA TGA AT--T AAT*
TAT* GCT* GAG T*GA T*AT* C-5',

40 where T* represents allylamine dU, and therefore ethidium modification and the 10 base sequence set off by dashes (--AA TCA TGA AT--) was introduced to provide a restriction enzyme site.

Example 16

45 Use of the Oligonucleotide 50-Mer to Regulate RNA Synthesis *In Vitro*

This nucleotide is complementary to the ATG strand of the lac z gene of IBI 31, and also contains a 10-base sequence for use in restriction enzyme digestion. The oligonucleotide 50-mer also contains sequences overlapping the T7 promoter in the IBI 31 plasmid constructs. Thus, it might be expected to interfere with *in vitro* transcription by T7 RNA polymerase even though the sequences in this oligo are entirely upstream of the start of transcription by T7 RNA polymerase. Because the plasmid constructs contain opposing T7 and T3 promoters, this also means that the oligo 50-mer is identical in sequence to the RNA that is made by the T3 RNA polymerase *in vitro*.

55 The effect of this oligonucleotide on *in vitro* transcription by T7 and T3 polymerases from an IBI 31 plasmid construct (pIBI 31-BH5-2) and from a BlueScript II plasmid construct (pBSII/HCV) was studied. See Figure 18 which contains the same target sequences, but in a "split" arrangement. The polylinker sequences of these plasmids are given in Figure 18. Comparing the effect of the oligo on these two

different target template serves to partially control for the possible non-specific inhibitory effects of ethidium groups on the RNA polymerases because the oligonucleotide would be expected to inhibit transcription from any template containing an appropriate promotor regardless of the "split" if the effect were due to the oligo's interaction with the polymerase rather than with the template.

At a concentration of 60-fold excess of oligonucleotide (0.6 μ M final) over plasmid with either the allylamine labeled oligonucleotide or the ethidium labeled oligonucleotide in a transcription reaction mixture, the following results were obtained:

Plasmid Transcribed	Polymerase Used	Oligo Used	nanomoles Incorporated	% of control
pIBI 31-BH5-2	T3	None	236	100
pIBI 31-BH5-2	T3	Allylamine labeled	233	99
pIBI 31-BH5-2	T3	Ethidium labeled	87	37
pIBI 31-BH5-2	T7	None	208	100
pIBI 31-BH5-2	T7	Allylamine labeled	198	95
pIBI 31BH-5-2	T7	Ethidium labeled	3	1.4
pBSII/HCV	T3	None	112	100
pBSII/HCV	T3	Allylamine labeled	158	>100
pBSII/HCV	T3	Ethidium labeled	185	>100
pBSII/HCV	T7	None	125	100
pBSII/HCV	T7	Allylamine labeled	154	>100
pBSII/HCV	T7	Ethidium labeled	62	50

These results indicate that the ethidium-modified oligo sequence is capable of specifically inhibiting transcription by the T7 polymerase from the T7 promotor region provided that the promotor region is not interrupted by the multiple cloning region and inserted DNA. Thus, the effect is dependent on the template DNA and is not merely the result of inhibition of the T7 polymerase by the ethidium groups.

Many obvious variations will be suggested to those of ordinary skill in the art in light of the above detailed description of the invention. All such variations are fully embraced by the scope and spirit of the present invention as set forth in the claims which follow.

Claims

1. An *in vitro* process for producing more than one copy of a specific nucleic acid, said process being independent of a requirement for the introduction of an intermediate structure for the production of said specific nucleic acid, said process comprising the steps of:
 - (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
 - (b) contacting said sample with a mixture comprising:
 - (i) nucleic acid precursors,
 - (ii) one or more specific nucleic acid primers each of which is complementary to a distinct sequence of said specific nucleic acid, and
 - (iii) an effective amount of a nucleic acid producing catalyst; and
 - (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing more than one copy of said specific nucleic acid.
2. An *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:
 - (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
 - (b) contacting said sample with a mixture comprising:
 - (i) nucleic acid precursors,
 - (ii) one or more specific polynucleotide primers comprising at least one ribonucleic acid segment each of which primer is substantially complementary to a distinct sequence of said specific nucleic acid, and
 - (iii) an effective amount of a nucleic acid producing catalyst; and

- (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and
 (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.
- 5
3. An *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:
- 10 (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
- (b) contacting said sample with a mixture comprising:
- (i) unmodified nucleic acid precursors,
- (ii) one or more specific chemically-modified primers each of which primer is substantially complementary to a distinct sequence of said specific nucleic acid, and
- 15 (iii) an effective amount of a nucleic acid producing catalyst; and
- (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and
- (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.
- 20
4. An *in vitro* process for producing more than one copy of a specific nucleic acid, said products being substantially free of any primer-coded sequences, said process comprising the steps of:
- 25 (a) providing a nucleic acid sample containing or suspected of containing the sequence of said specific nucleic acid;
- (b) contacting said sample with a mixture comprising:
- (i) unmodified nucleic acid precursors,
- (ii) one or more specific unmodified primers comprising at least one segment each of which primer comprises at least one non-complementary sequence to a distinct sequence of said specific nucleic acid, such that upon hybridization to said specific nucleic acid at least one loop structure is formed, and
- 30 (iii) an effective amount of a nucleic acid producing catalyst; and
- (c) allowing said mixture to react under isostatic conditions of temperature, buffer and ionic strength, thereby producing at least one copy of said specific nucleic acid; and
- 35 (d) removing substantially or all primer-coded sequences from the product produced in step (c) to regenerate a primer binding site, thereby allowing a new priming event to occur and producing more than one copy of said specific nucleic acid.
5. A promoter-independent non-naturally occurring nucleic acid construct which when present in a cell produces a nucleic acid without the use of any gene product coded by said construct.
- 40
6. A conjugate comprising a protein-nucleic acid construct, said nucleic acid construct not coding for said protein, and which conjugate produces a nucleic acid when present in a cell.
- 45
7. An *in vivo* process for producing a specific nucleic acid, said process comprising the steps of:
- (a) providing a conjugate comprising a protein-nucleic acid construct, said conjugate being capable of producing a nucleic acid when present in a cell; and
- (b) introducing said conjugate into a cell, thereby producing said specific nucleic acid.
- 50
8. A construct comprising a host promoter located on the construct such that the host transcribes a sequence in the construct coding for a different RNA polymerase which after translation is capable of recognizing its cognate promoter and transcribing from a DNA sequence of interest in the construct with said cognate promoter oriented such that it does not promote transcription from the construct of said different RNA polymerase.
- 55

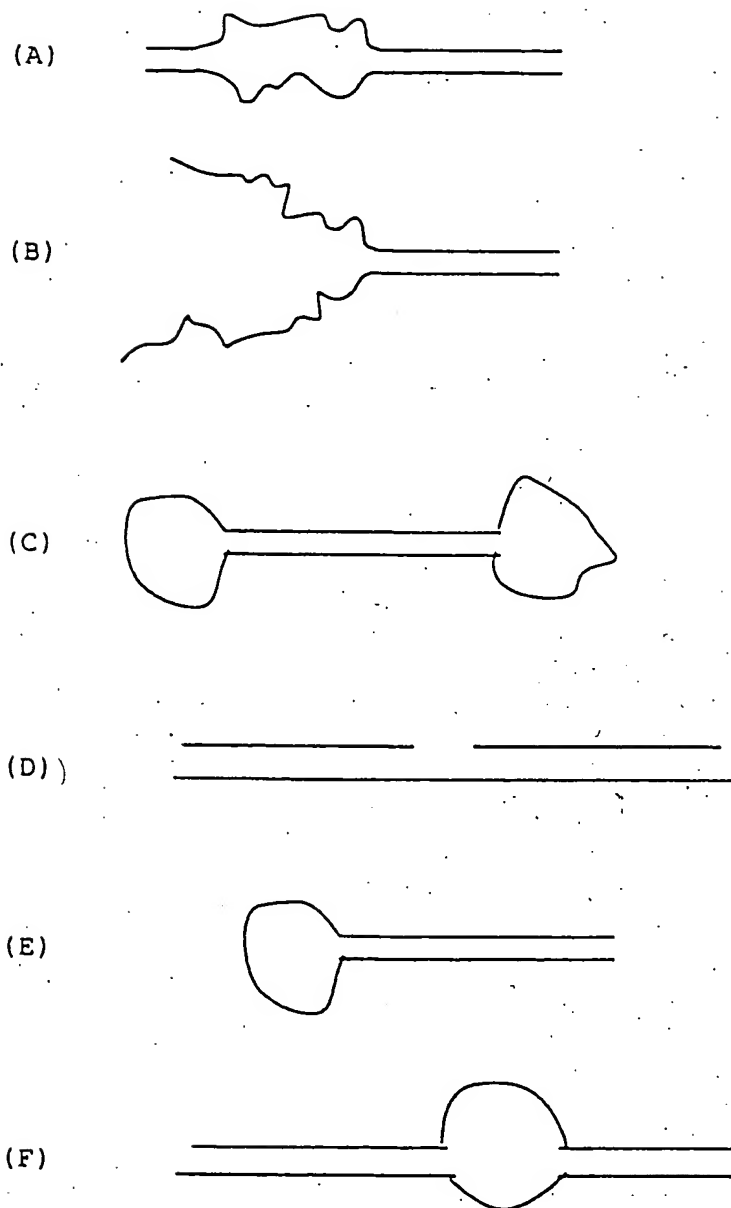


Figure 1 (A-F)

Construct Forms Comprising at Least one Single-Stranded Region

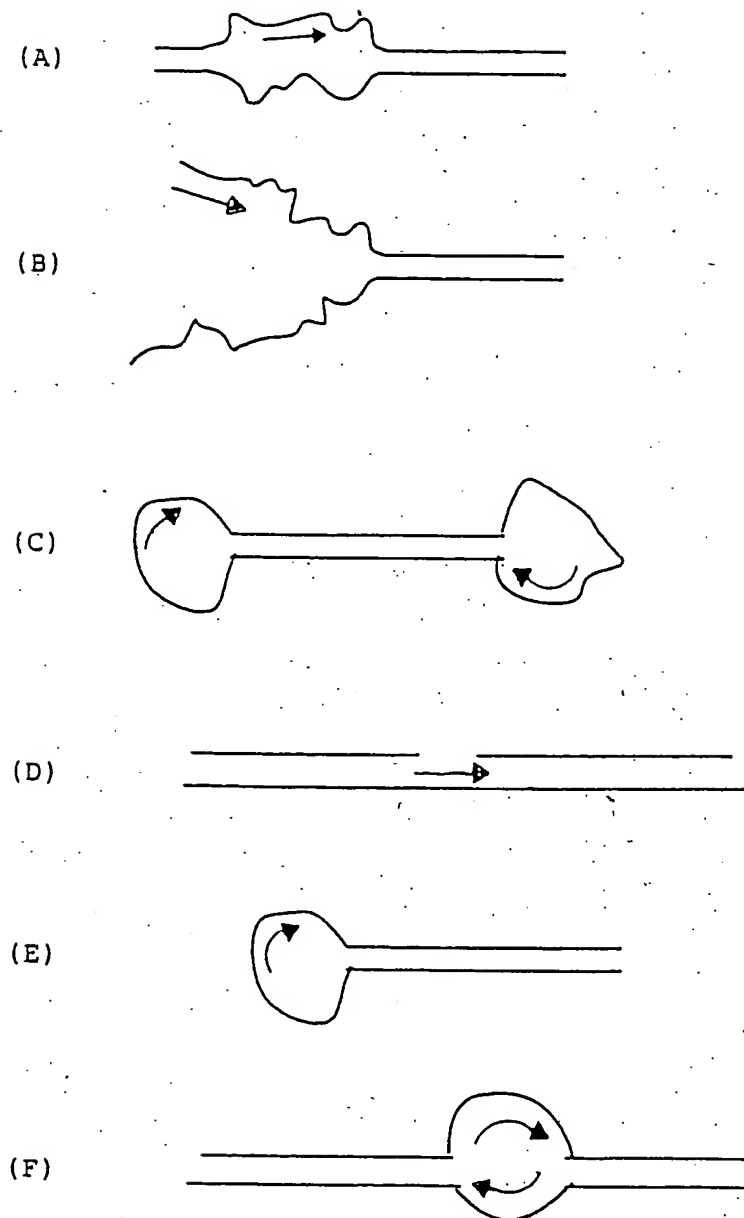


Figure 2 (A-F)

Functional Forms of the Construct

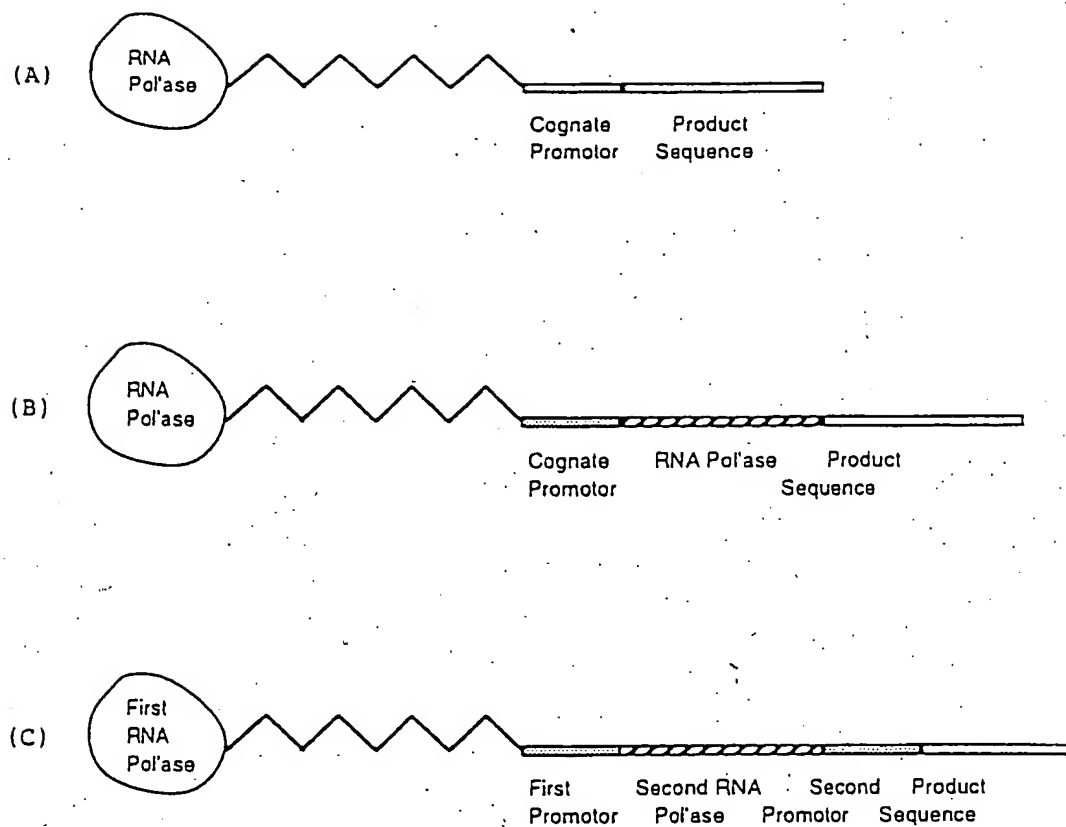


Figure 3 (A-C)

Three Constructs with an RNA Polymerase
Covalently Attached to a Transcribing Cassette

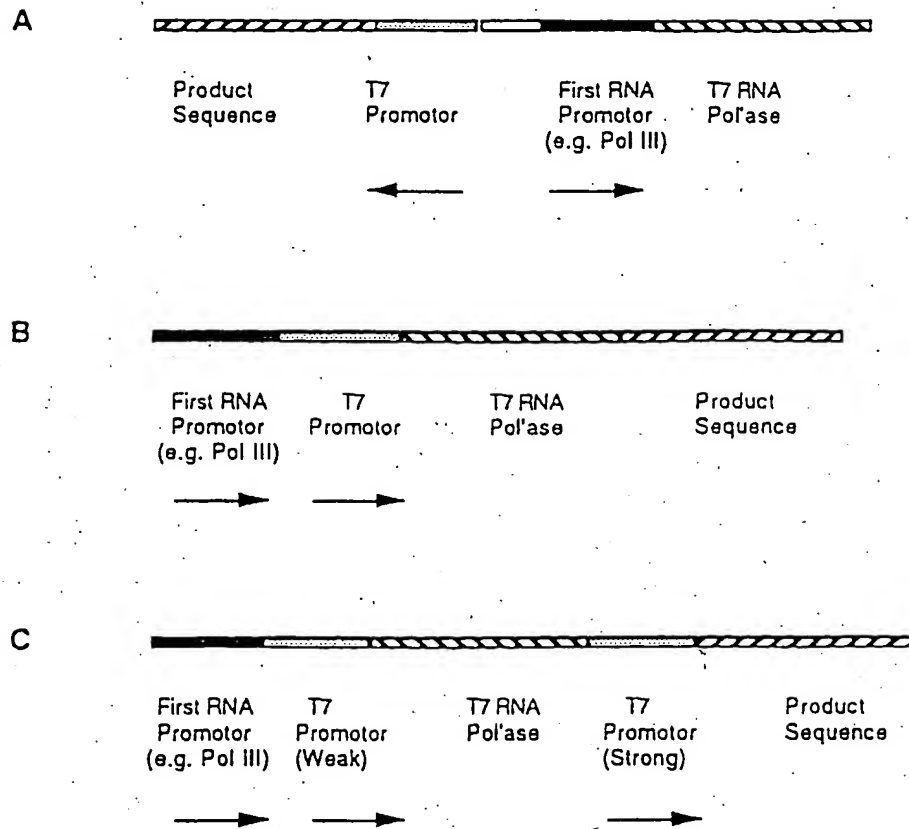


Figure 4 (A-C)

Three Constructs with Promoters
for Endogenous RNA Polymerase

M13mp18. Seq Length: 7250

1.	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTOGG00000
51.	AAATGAAAAT	ATAGCTAAAC	AGGTATTGA	OCATTTGOGA	AATGTATCTA
101.	ATGGTCAAAC	TAAATCTACT	CGTTGCGAGA	ATTGGGAATC	AACTGTTACA
151.	TGGAATGAAA	CTTCCAGACA	COGTACTTTA	GTTGCATATT	TAAAACATGT
201	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGOCA	TCCGCAAAAA
251	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TOCTGACCTG
301.	TTGGAGTTTG	CTTCCGGTCT	GGTTGCGCTT	GAACTCGAA	TTAAAACGGG
351.	ATATTTGAAG	TCTTTGGGGC	TTCCTCTTAA	TCTTTTGTAT	GCAATCCGCT
401.	TTGCTTCTGA	CTATAATAGT	CAGGGTAAAG	ACCTGATTTT	TGATTATGGG
451.	TCACTCTCGT	TTTCTGAAGT	GTTTAAAGCA	TTTGAGGGGG	ATTCAATGAA
501.	TATTTATGAC	GATTCGCGAG	TATTGGACGC	TATCCAGTCT	AAACATTTTA
551.	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT
601.	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC
651.	TATGCTCGT	AATTCCTTTT	GGGTTATGT	ATCTGCATTA	GTTGAATGTG
701.	GTATTOCTAA	ATCTCAACTG	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT
751.	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	TCTTCCCAAC	GTCCTGACTG
801.	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	CAATGATTAA
851.	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTC
901.	TCGTCAGGGC	AAGCTTATT	CACTGAATGA	GCAGCTTTGT	TACGTTGATT
951.	TGGGTAATGA	ATATCCGGTT	CTTGTGGAAG	ATTACTCTTG	ATGAAGGTCA
1001	GCCAGCCTAT	GCGCCTGGTC	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG
1051	TTGGTCAGTT	CGGTTCCCTT	ATGATTGAAC	GTCTGCGCCT	CGTTCCGGCT
1101	AAGTAACATG	GAGCAGGTGG	CGGATTTGGA	CACAATTTAT	CAGGCGATGA
1151	TACAAATCTC	CGTTGTACCTT	TGTTTGGGCG	TTGGTATAAT	CGCTGGGGGT
1201	CAAAGATGAG	TGTTTTAGTG	TATTCTTTGG	CCTCTTTCGT	TTTAGGTTGG

Figure 5

M13mp18 Nucleic Acid Sequence

1251	TGCTTCGTGTA	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC
1301	ATGAAAAAGT	CTTTAGTCT	CAAAGCCTCT	GTAGCGGTG	CTAAGCTCGT
1351	TCGATGCTG	TCTTTCGTG	CTGAGGGTGA	CGATCGGCA	AAAGGGGCT
1401	TTAACTCCT	GCAAGCTCA	GCGACGAAT	ATATCGGTTA	TGGTGGGGG
1451	ATGGTTGTG	TCATTGTGG	CGCAACTATC	GGTATCAAGC	TGTTAAGAA
1501	ATTCACTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCTTTT
1551	GGAGCTTTT	TTTTTGGAGA	TTTCAAAGT	GAAAAAATTA	TTATTCGCAA
1601	TTCTTTAGT	TGTTCTTTT	TATTCTCACT	CGCTGAAAC	TGTTGAAAGT
1651	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	TTTACTAAG	TCTGGAAAGA
1701	CGACAAAAGT	TTAGATGTT	ACGCTAACTA	TGAGGGTTGT	CTGTGGAATG
1751	CTACAGGGT	TGTAGTTGT	ACTGGTGAAG	AAACTCAGTG	TTACGGTACA
1801	TGGGTTCCTA	TTGGCTTGC	TATCCTGAA	AATGAGGGTG	GTGGCTCTGA
1851	GGGTGGGGT	TCTGAGGGT	GCGTTCTGA	GGGTGGGGT	ACTAAAGCTC
1901	CTGAGTAAGG	TGATACACT	ATTGCGGGT	ATACTTATAT	CAAGCTCTC
1951	GAGGGCACTT	ATCGGCTGG	TACTGAGCAA	AACCGGCTA	ATCCTAATCC
2001	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	CAGAATAATA
2051	GGTTGGAAG	TAGGCAGGG	GCATTAAGTG	TTTATACGGC	CAGTGTACT
2101	CAAGGCCTG	AACCGGTTAA	AACTTATTAC	CAGTACCTC	CTGTATCATC
2151	AAAAGGCATG	TATGAGCTT	ACTGGAAGG	TAAATTCAGA	GCTGGGCTT
2201	CAAGGCCTG	AACCGGTTAA	AACTTATTAC	CAGTACCTC	CTGTATCATC
2251	AAAAGGCATG	TGCTCAAGC	TCTGTCAAT	GCTGGGGGG	GCTGTGGTGG
2301	TGCATTCTGG	CTTTAATCAA	GATCCATTGG	TTTGTGAATA	TCAAGGCCAA
2351	TGCTCTGAAG	TGCTCAAGC	TCTGTCAAT	GCTGGGGGG	GCTGTGGTGG
2401	TGGTCTGGT	GGGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	GGGGGTTCTG
2451	AGGGTGGGG	CTCTGAGGGA	GGGGTTTGG	GTGGTGGCTC	TGGTTCCGGT
2501	GATTTTGATT	ATGAAAAGAT	GGCAAGGCT	AATAAGGGGG	CTATGACCGA
2551	AAATGCGGAT	GAAAAAGGCG	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT

Figure 5

M13mp18 Nucleic Acid Sequence

2501	CTGTGGCTAC	TGATTACGGT	GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT
2551	TGCGGCGTTG	CTAATGGTAA	TGGTGCTACT	GGTGATTTTG	CTGGCTCTAA
2601	TTGCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	TTAATGAATA
2651	ATTTCGGTCA	ATATTTACCT	TOOCTOCTC	AATCGGTTGA	ATGTGCGOCT
2701	TTTGTCTTTA	GCGCTGGTAA	AOCATATGAA	TTTTCTATTG	ATTGTGACAA
2751	AATAAACTTA	TTCGGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT
2801	TTATGTATGT	ATTTTCTACG	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT
2851	TTATCATGOC	AGTTCTTTTG	GGTATTCOGT	TATTATTGCG	TTTCTCGGTT
2901	TTCCTTCTGG	TAACCTTGTT	CGGCTATCTG	CTTACTTTTC	TAAAAAGGG
2951	CTTCGGTAAG	ATAGCTATTG	CTATTTCAAT	GTTTCTTGCT	CTTATTATTG
3001	GGCTTAACTC	AATTCTTG TG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA
3051	COCTCTGACT	TTGTTACGGG	TGTTACGTTA	ATTCTOOGT	CTAATGCGCT
3101	TCOCTGTTTT	TATGTTATTC	TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG
3151	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	ATTGGGATAA	ATAATATGGC
3201	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGAGG	CTOGTTAGCG
3251	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT
3301	CTTGATTAA	GGCTTCAAAA	OCTOOGCAA	GTOGGGAGGT	TOGCTAAAAC
3351	GOCTOGCGTT	CTAGAATAC	CGGATAAGOC	TTCTATATCT	GATTTGCTTG
3401	CTATTEGGOG	CGGTAATGAT	TOCTAOGAATG	AAAATAAAAA	CGGCTTGCTT
3451	GTTCTOGATG	AGTGOGGTAC	TTGGTTTAAT	ACCOGTTCTT	GGAATGATAA
3501	GGAAAGACAG	COGATTATTG	ATTGGTTTCT	ACTGCTOGT	AAATTAGGAT
3551	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTOGTGTC	TGGACAGAAT
3651	TACTTTACCT	TTTGTGGTA	CTTTATATTC	TCTTATTACT	GGCTOGAAAA
3701	TGCTCTGOC	TAAATTACAT	GTTGGCGTTG	TAAATATGG	CGATTCTCAA
3751	TTAAGCOCTA	CTGTTGAGCG	TTGGCTTTAT	ACTGTAAGA	ATTGTATAA
3801	CGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	TCGGTGTTT

Figure 5

M13mp18 Nucleic Acid Sequence

3851	ATTCTTATTT	AACGCCCTTAT	TTATCACAAG	GTOGGTATTT	CAAAOCATTA
3901	AATTTAGGTC	AGAAGATGAA	ATTAAGTAAA	ATAATATTGA	AAAAGTTTTC
3951	TOGOGTTCTT	TGTCTTGOGA	TTGGATTTGC	ATCAGCATT	ACATATAGTT
4001	ATATAACCCA	AOCTAAGCOG	GAGGTTAAAA	AGGTAGTCTC	TCAGAOCCTAT
4051	GATTTTGATA	AATTCACAT	TGACTCTTCT	CAGOGTCTTA	ATCTAAGCTA
4101	TOGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	AGCGOGATT
4151	TACAGAAGCA	AGGTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC
4201	ATTAATAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT
4251	TCTTGATGTT	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT
4301	AATTOGCTC	TGOGOGATTT	TGTAACCTGG	TATTCAAAGC	AATCAGGOGA
4351	AATCGGTTATT	GTTTCTCOOG	ATGTAAAAGG	TACTGTTACT	GTATATTCAT
4401	CTGAOGTTAA	AOCTGAAAAT	CTACGCAATT	TCTTTATTTT	TGTTTACGT
4451	GCTAATAATT	TTGATAATGGT	TGGTTCAATT	OCTTCCATAA	TTCAGAAGTA
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC
4551	AGGAATATGA	TGATAATTCC	GCTOCTTCTG	GTGGTTTCTT	TGTTCCGCAA
4601	AATGATAATG	TTACTCAAAC	TTTTAAAATT	AATAACGTTT	GGGCAAGGA
4651	TTTAATACGA	GTTGTGGAAT	TGTTTGTAAG	GTCTAATACT	TCTAAATCCT
4701	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	TAGTGCTCCT
4751	AAAGATATTT	TAGATAAOCCT	TOCTCAATTC	CTTTCTACTG	TTGATTTGOC
4801	AACTGAOCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG
4851	ATGCTTTAGA	TTTTTCATTT	GCTGCTGGCT	CTCAGGTGG	CACTGTTGCA
4901	GGGGTGTGA	ATACTGAOCG	OCTCAOCTCT	GTTTTATCTT	CTGCTGGTGG
4951	TTGGTTGGGT	ATTTTAAATG	GCGATGTTTT	AGGGCTATCA	GTTCCGGCAT
5001	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCAAG	TATCTTAACG
5051	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT
5101	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCAAG	TATCTTAACG
5151	CGATTGAGCG	TCAAAATGTA	GGTATTTCCA	TGAGOGTTTT	TOCTGTTGCA

Figure 5

5201	ATGGCTGGGG	GTAATATTGT	TCTGGATATT	AOCAGCAAGG	CCGATAGTTT
5251	GAGTTCTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA	AGAAGTATTG
5301	CTACAAOGGT	TAATTTGOGT	GATGGACAGA	CTCTTTTACT	CGGTGGGCTC
5351	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGGTAAOOGT	TCCTGTCTAA
5401	AATCCCTTTA	ATGGGCTOC	TGTTTAGCTC	CCGCTCTGAT	TCCAAAGAGG
5451	AAAGCAOGTT	ATAOGTGCTC	GTCAAAGCAA	CCATAGTAOG	CGOOCGTGTAG
5501	CGGGGCATTA	AGGGGGGGGG	GTGTGGTGGT	TACGGGCAGC	GTGACGGCTA
5551	CACTTGOCAG	CGOOCAGGG	CCGGCTOCTT	TCGCTTTCTT	CCCTTCCTTT
5601	CTGGCCAOGT	TGGGGGGCTT	TCCCGTCAA	GCTCTAAATC	GGGGGGTCCC
5651	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCCGACCCCG	AAAAAACTTG
5701	ATTTGGGTGA	TGGTTCAOGT	AGTGGGOCAT	CGOOCGTGATA	GAOGGTTTTT
5751	CGOOCCTTGA	CGTTGGAGTC	CAOGTTCTTT	AATAGTGGAC	TCTTGTTCOA
5801	AACTGGAACA	ACACTCAAOC	CTATCTGGGG	CTATTCTTTT	GATTTATAAG
5851	GGATTTTGOC	GATTTGGGAA	CCACCATCAA	ACAGGATTTT	CGCTGCTGG
5901	GGCAAACAG	CGTGGACGGC	TTGCTGCAAC	TCTCTCAGGG	CCAGGGGGTG
5951	AAGGGCAATC	AGCTGTTGOC	CGTCTGGCTG	GTGAAAAGAA	AAACCAOOGT
6001	GGGGCCCAAT	AOGCAAAOOG	OCTCTCCOOG	CGGGTTGGGC	GATTCATTAA
6051	TGCAGCTGGC	AOGACAGGTT	TCCCGACTGG	AAAGGGGGCA	GTGAGGGCAA
6101	CGCAATTAAT	GTGAGTTAGC	TCACTCATTAA	GGCACCCAG	GCTTTACACT
6151	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGGG	ATAACAATTT
6201	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTOGAGC	TGGGTACCGG
6251	GOGATCTCT	AGAGTGGAC	TGCAGGCATG	CAAGCTTGGC	ACTGGGCGTC
6301	GTTTTACAAC	GTGTGACTG	GGAAAAOOGT	GGGGTTACCC	AACTTAATOG
6351	CCTTGACGCA	CAATCCOCTT	TGGCCAGCTG	GCGTAATAGC	GAGAGGGGCC
6401	GCAOOGATCG	CCCTTCCCAA	CAGTTGGGCA	GCGTGAAATG	CGAATGGGGC
6451	TTTGCGTGGT	TTGGGGCAC	AGAGGGGGTG	CCGGAAAGCT	GGCTGGAGTG
6501	CGATCTTCT	GAGGGCGATA	CGGTGGTGGT	CCOCTCAAAC	TGGCAGATGC

Figure 5

M13mp18 Nucleic Acid Sequence

6551	ACGGTTAOGA	TGOGGOCATC	TACAACAAOG	TAACCTATOC	CATTACGGTC
6601	AATCGGCGGT	TTGTTCCAC	GGAGAATCOG	ACGGGTTGTT	ACTOGCTCAC
6651	ATTTAATGTT	GATGAAAGCT	GGCTACAGGA	AGGOCAGACG	CGAATTATTT
6701	TTGATGGCGT	TCCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA
6751	ACGOGAATTT	TAACAAAATA	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT
6801	ACAATCTTCC	TGTTTTTGGG	GCTTTTCTGA	TTATCAACCG	GGGTACATAT
6851	GATTGACATG	CTAGTTTTAC	GATTACGGTT	CATCGATTCT	CTTGTTTGCT
6901	CCAGACTCTC	AGGCAATGAC	CTGATAGCCT	TTGTAGATCT	CTCAAAAATA
6951	GCTACCCCTCT	CCGGCATGAA	TTTATCAGCT	AGAACGGTTG	AATATCATAT
7001	TGATGGTGAT	TTGACTGTCT	CCGGCCTTTC	TCACCCCTTT	GAATCTTTAC
7051	CTACACATTA	CTCAGGCATT	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT
7101	TTTTATCCTT	GCGTTGAAAT	AAAGGCTTCT	CCCGCAAAAG	TATTACAGGG
7151	TCATAATGTT	TTTGGTACAA	CCGATTTAGC	TTTATGCTCT	GAGGCTTTAT

Figure 5

M13mp18 Nucleic Acid Sequence

COMPLEMENTARY TO M₁₃

POSITION	5' . . . 3'	POSITION	
645	AGCAACACTATCATA	631	M ₁₃ /1
615	ACGACGATAAAAAACC	601	M ₁₃ /2
585	TTTTGCAAAAGAAGT	571	M ₁₃ /3
555	AATAGTAAATGTTT	541	M ₁₃ /4
525	CAATACTGCGGAATG	511	M ₁₃ /5
495	TGAATCCCCCTCAAA	481	M ₁₃ /6
465	AGAAAACGAGAATGA	451	M ₁₃ /7
435	CAGGTCTTTACCGTG	421	M ₁₃ /8
405	AGGAAAGCGGATTGC	391	M ₁₃ /9
375	AGGAAGCCCGAAAGA	361	M ₁₃ /10

COMPLEMENTARY TO SS PHAGE DNA

POSITION	5' . . . 3'	POSITION	
351	ATATTGAAGTCTTT	366	M ₁₃ /11
371	TCTTTTGGATGCAAT	386	M ₁₃ /12
391	CTATAATACTCAGGG	406	M ₁₃ /13
411	TGATTATGGTCATT	426	M ₁₃ /14
431	GTTTAAAGCATTGA	446	M ₁₃ /15
451	TATTATGACGATTG	466	M ₁₃ /16
471	TATCCAGTCTAAACA	486	M ₁₃ /17
491	CTCTGGCAAACTTC	506	M ₁₃ /18
511	TCGCTATTTGGTTT	526	M ₁₃ /19
531	AAACGAGGGTTATGA	546	M ₁₃ /20

Figure 6

Primers for Nucleic Acid Production
Derived from M13mp18 Sequence

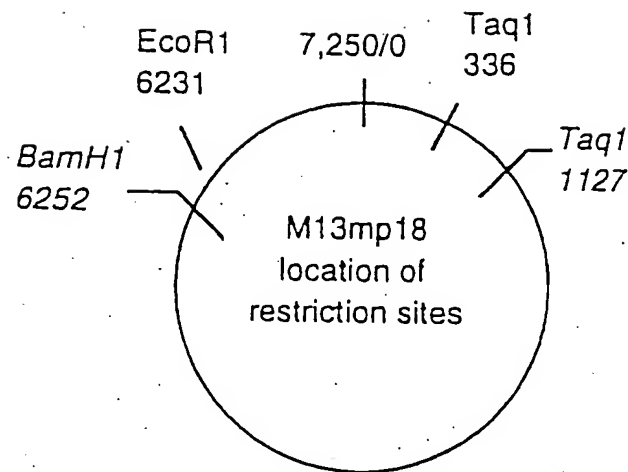


Figure 7

Appropriate M13mp18 Restriction Sites



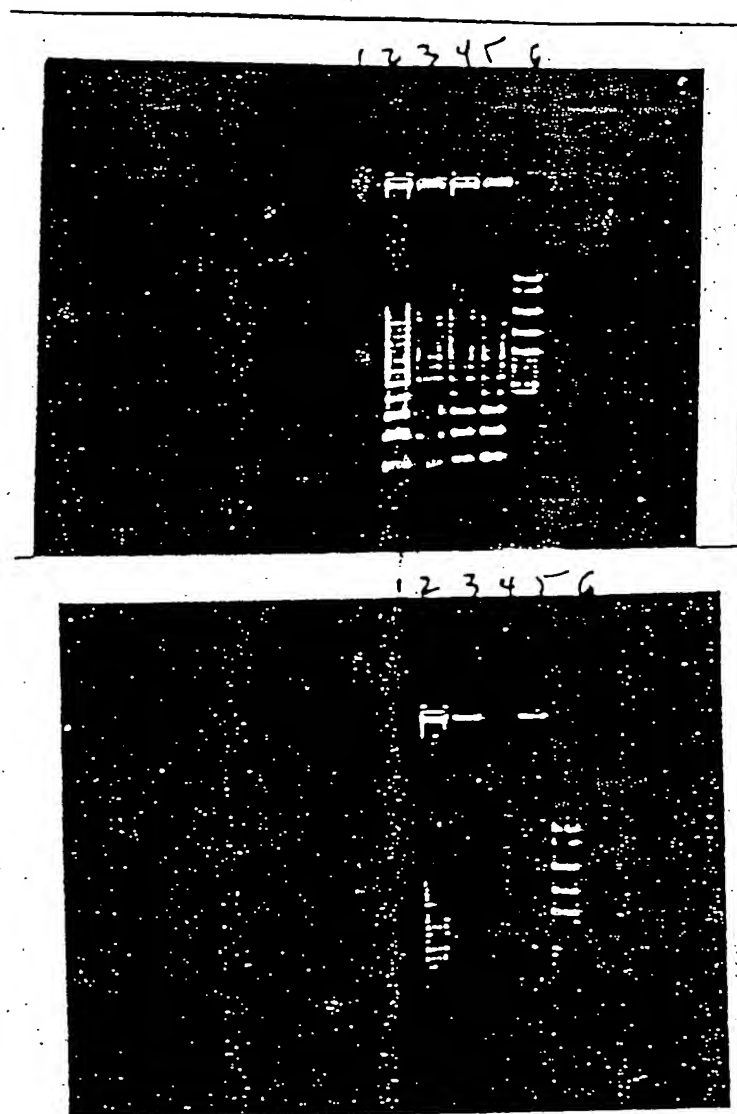
Lane 1: from calf thymus + Taq digested mp18 amplification reaction
Lane 2: from Taq digested mp18 amplification reaction
Lane 3: from calf thymus amplification reaction
Lane 4: øX174 Hinf1 size marker

Figure 8



Lane 1: no template
Lane 2: mp18 template, phosphate buffer
Lane 3: MspI/pBR322 size marker
Lane 4: mp18 template, MOPS buffer

Figure 9



Top= (+) Template

Bottom= (-) Template

Lane 1: phosphate buffer

Lane 2: MES

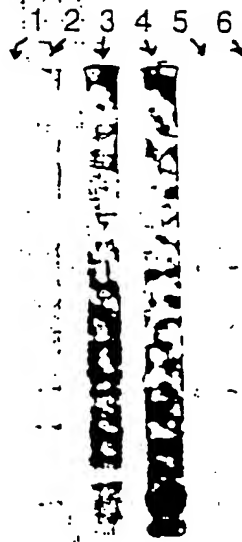
Lane 3: MOPS

Lane 4: DMAB

Lane 5: DMG

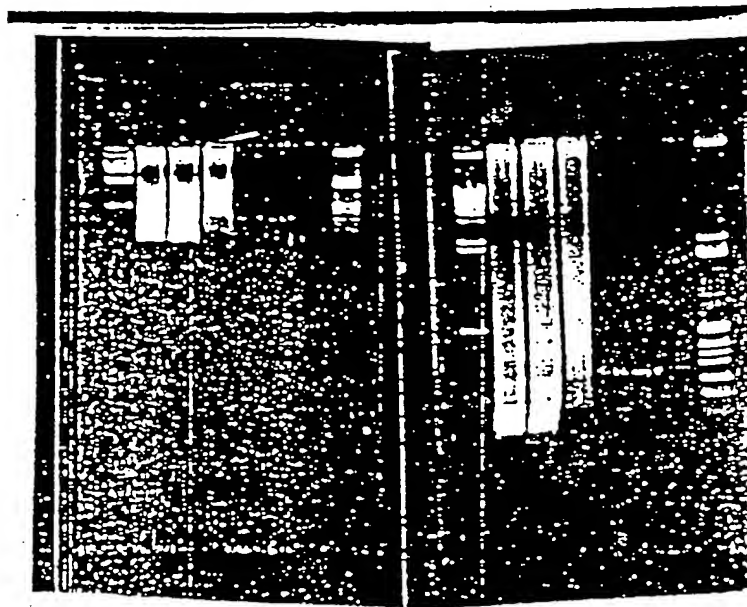
Lane 6: pBR322/Mspl size marker

Figure 10



Lane 1: DMAB buffer, no template
Lane 2: DMAB buffer, mp18 template
Lane 3: DMG buffer, no template
Lane 4: DMG buffer, mp18 template
Lane 5: No reaction
Lane 6: 200 ng Taq I digested mp18
size marker/positive control

Figure 11



First Time Interval Second Time Interval

Agarose Gel Analysis

- Lane 1: lambda Hind III marker
- Lane 2: Amp/Untreated
- Lane 3: Amp/Kinased
- Lane 4: Amp/Kinased/Ligated
- Lane 5: PCR/Untreated
- Lane 6: PCR/Kinased
- Lane 7: PCR/Kinased/Ligated
- Lane 8: ϕ X174/Hinf1 marker

Figure 12

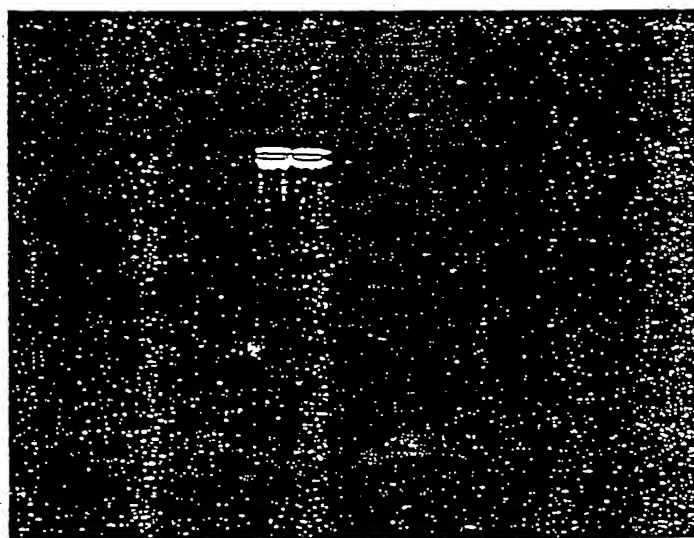
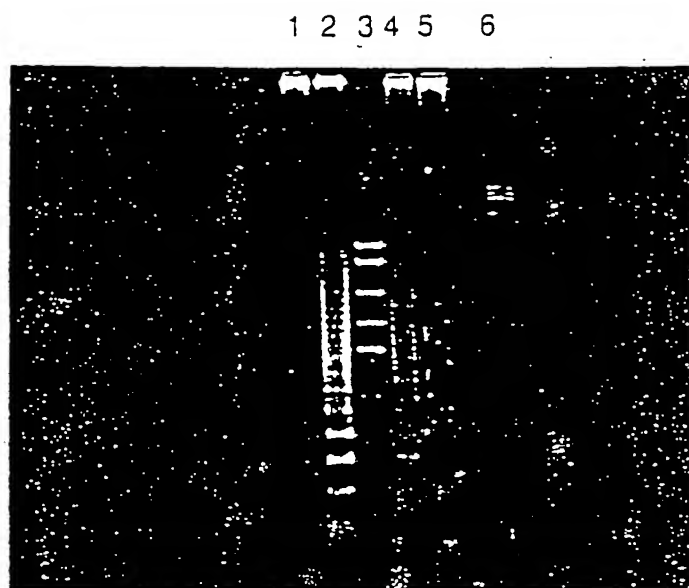
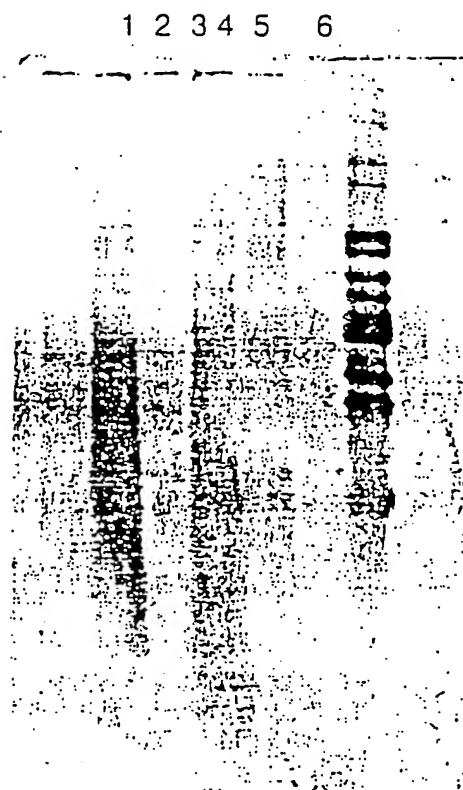


Figure 13



Lane 1: Primers alone
Lane 2: Primers + taq digested M13 DNA
Lane 3: Molecular weight markers
Lane 4: Primers + RNA
Lane 5: Primers alone
Lane 6: M13 digested DNA
Buffer was dimethyl amino glycine, pH 8.6

Figure 14



Lane 1: Primers alone
Lane 2: Primers + taq digested M13 DNA
Lane 3: Molecular weight markers
Lane 4: Primers + RNA
Lane 5: Primers alone
Lane 6: M13 digested DNA
Buffer was dimethyl amino glycine, pH 8.6

Figure 15

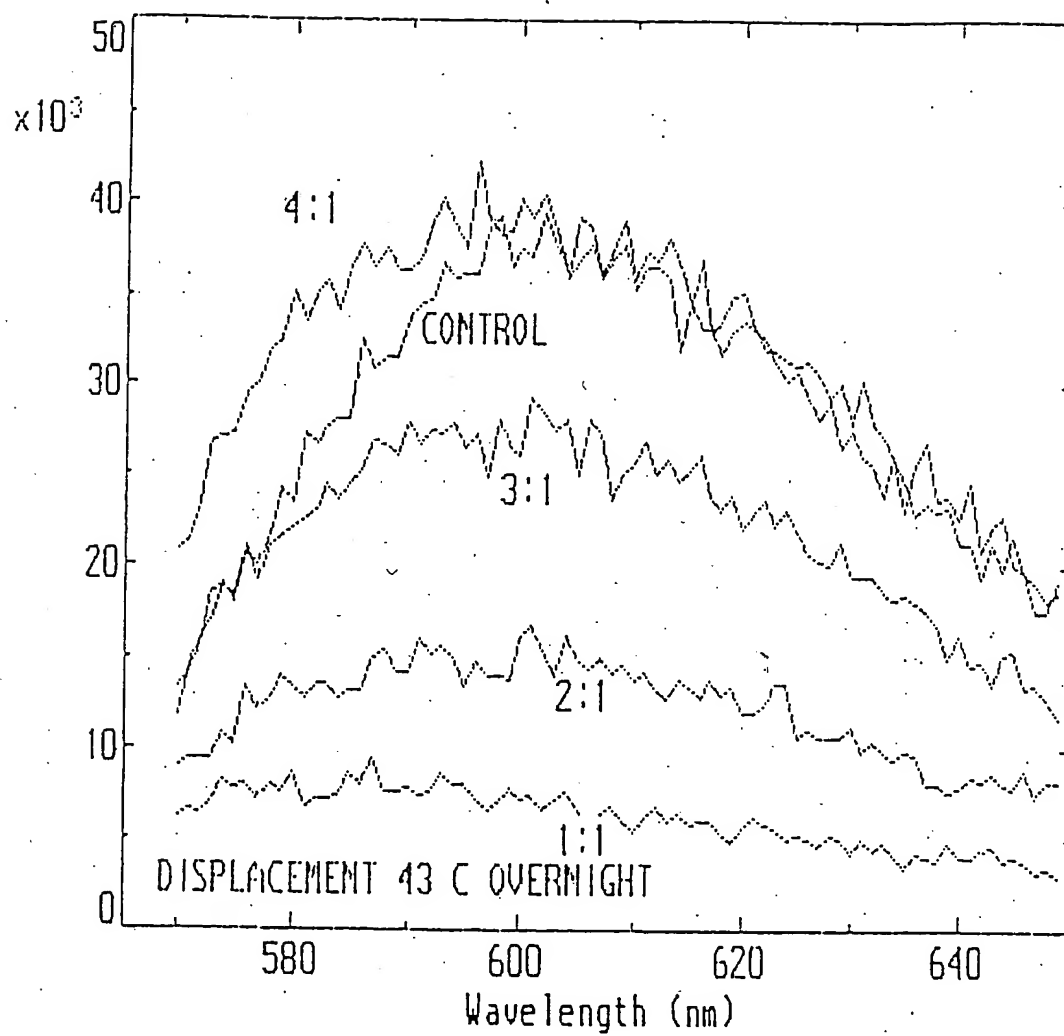


Figure 16

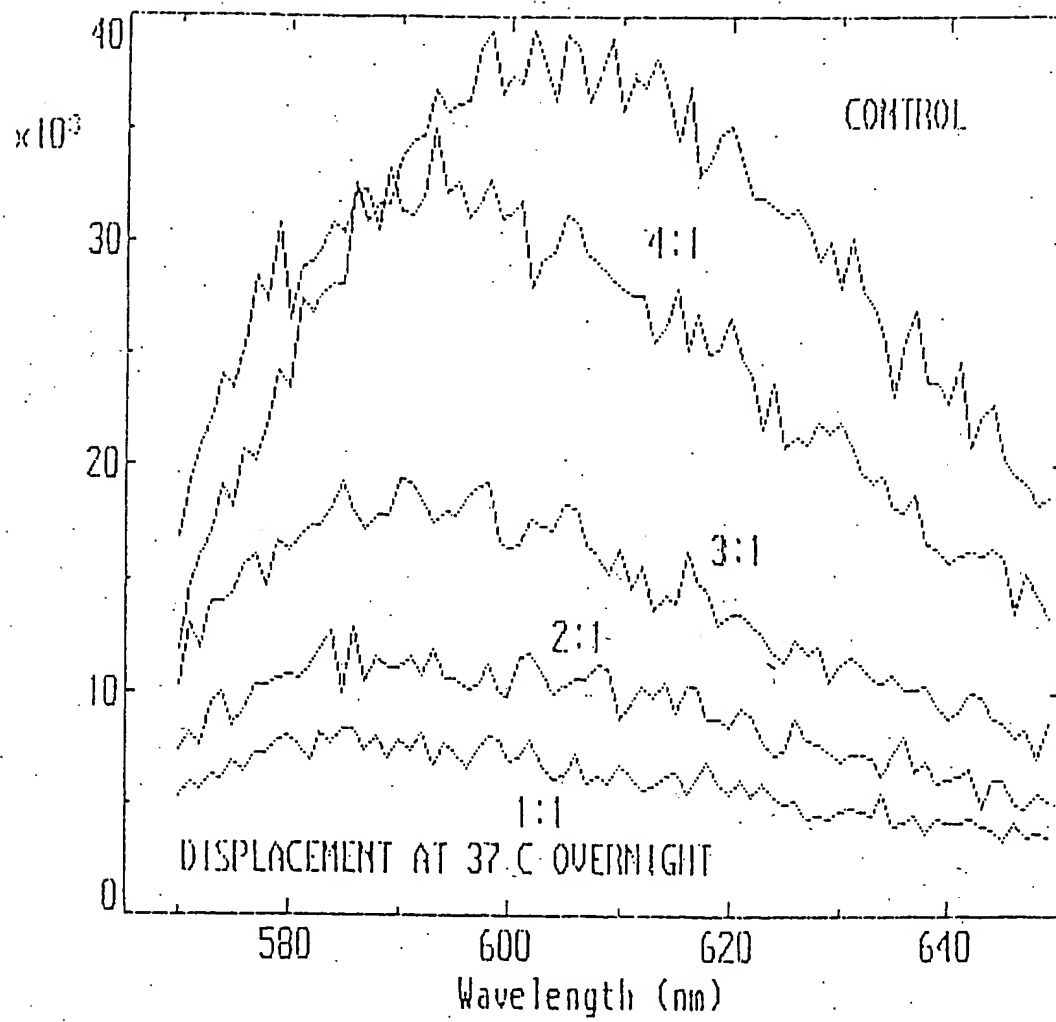


Figure 17

pIBI 31-BH5-2

fmet AUG of Lac z (T7 Promotor region....
 LAC PROMOTOR..ATG ACC ATG ATT ACG CCA GAT ATC AAA TTA ATA CGA CTC ACT ATA

oligo 50-mer 3'- tac t'aa t'gc ggt' ct'a t'ag t'Vt aat' tat' gct' gag t'ga t'at' c-5'
 10 base insert

T7 RNA Start (T7 Promotor Region)
 IGGG CTC ICCT TTA GTG ACG GTT AAT-
} T7 Start Signal

pIBI 31 BSII/HCV

fmet AUG of Lac z (T3 Promotor region --) T3 RNA Start
 LAC PROMOTOR ..ATG ACC ATG ATT ACG CCA AGC TCG AAA TTA ACC CTC ACT AAA /GGG

oligo 50-mer 3'- tac t'aa t'ac t'aa t'gc ggt' t'V--10 base insert--.....

{T7 Promotor Region }
 MULTIPLE CLONING SITE + 390 BASE INSERT CTA /TAG TGA GTC CGT ATT AAT....
 T7 Start Signal
 5'-ct'a t'ag t'ga gt'c gt'a tt'a at'.....

Figure 18